> 0 <
0| |0 IntelliGenetics
> 0 <

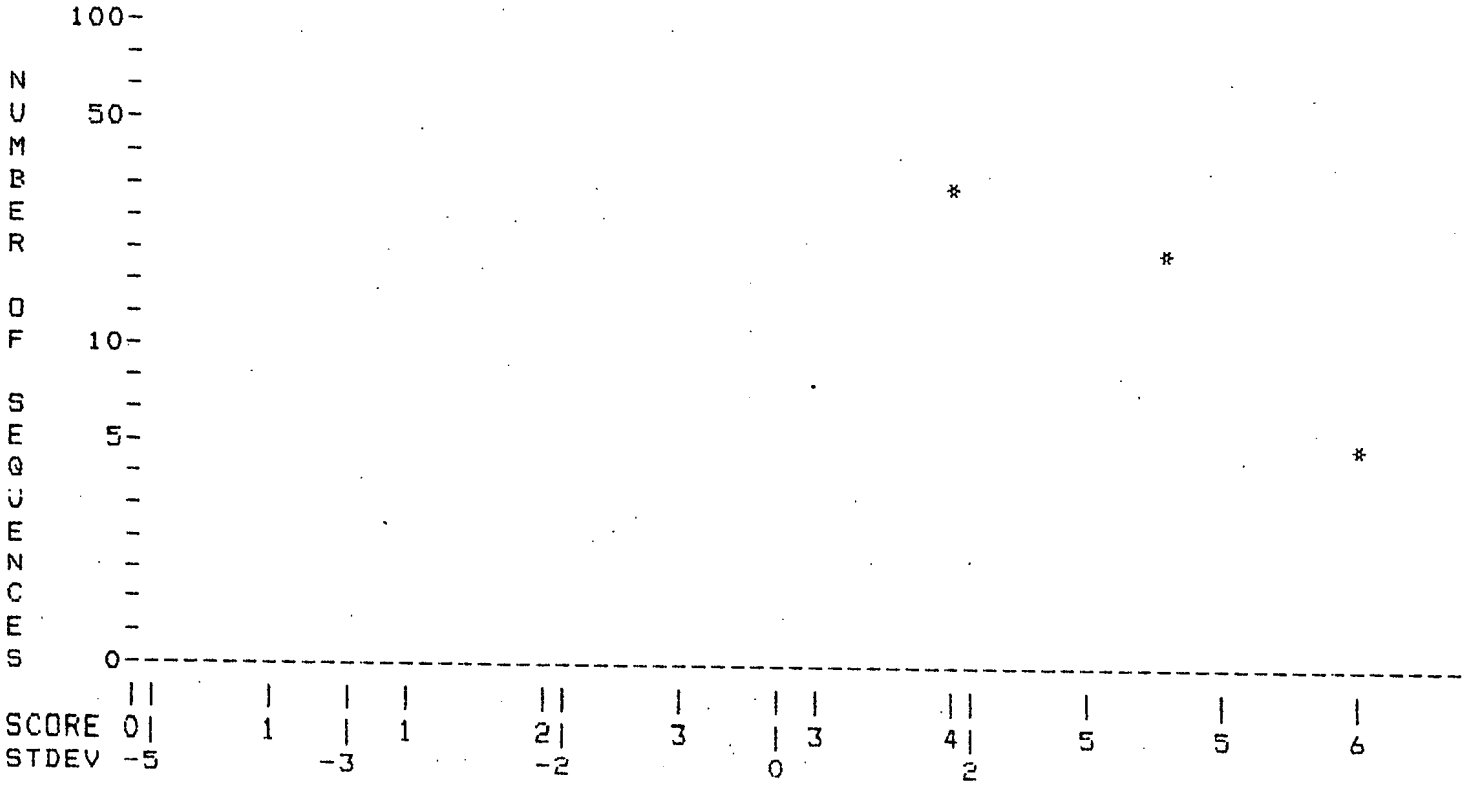
FastDB --Fast PairWise Comparison of Sequences
Release 5.4

sequences numbered as in table 4 1-19 (not by seq ID #)

Results file celsa-1-align.res made by alexk on Thu 25 Feb 93 10:46:11-PST.

Query sequence being compared: CELSA-1 (1-6)
Number of sequences searched: 50
Number of scores above cutoff: 50

Results of the initial comparison of CELSA-1 (1-6) with:
File : celsa-1.pep



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	4	5	0.65

Times:	CPU	Total Elapsed
	00:00:00.03	00:00:01.00

Number of residues:	30314
Number of sequences searched:	50
Number of scores above cutoff:	50

Significance is calculated based on initial score.

4 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. GNWVNE	Genome polyprotein - Tick-bor	3414	6	6	3.09	0
2. POLG_TBEVW	GENOME POLYPROTEIN (CONTAINS:	3414	6	6	3.09	0
3. GNWVTB	Genome polyprotein - Tick-bor	3412	6	6	3.09	0
4. POLG_TBEVS	GENOME POLYPROTEIN (CONTAINS:	3412	6	6	3.09	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
5. A39246	*Carboxypeptidase A precursor	417	5	5	1.55	0
6. CBPC_HUMAN	MAST CELL CARBOXYPEPTIDASE A	417	5	5	1.55	0
7. S04912	*yopA protein - Yersinia ente	455	5	5	1.55	0
8. A39938	*Phosphotransferase system en	460	5	5	1.55	0
9. PT2S_BACSU	PHOSPHOTRANSFERASE ENZYME II,	460	5	5	1.55	0
10. WMBE71	UL13 protein - Human herpesvi	518	5	5	1.55	0
11. D30083	*Gene UL13 protein - Human he	518	5	5	1.55	0
12. KR2_HSV11	PROBABLE SERINE/THREONINE-PRO	518	5	5	1.55	0
13. DNBEV1	DNA-binding protein - Human h	1196	5	5	1.55	0
14. DNBEKS	DNA-binding protein - Human h	1196	5	5	1.55	0
15. DNBEHF	DNA-binding protein - Human h	1196	5	5	1.55	0
16. B30085	*Gene UL29 protein (major DNA	1196	5	5	1.55	0
17. DNBI_HSV11	MAJOR DNA-BINDING PROTEIN.	1196	5	5	1.55	0
18. DNBI_HSV1F	MAJOR DNA-BINDING PROTEIN.	1196	5	5	1.55	0
19. DNBI_HSV1K	MAJOR DNA-BINDING PROTEIN.	1196	5	5	1.55	0
20. S19926	*Hypothetical protein - Red c	1864	5	5	1.55	0

1. CELSA-1 (1-6)
   GNWVNE Genome polyprotein - Tick-borne encephalitis virus

```
ENTRY           GNWVNE      #Type Protein
TITLE           Genome polyprotein - Tick-borne encephalitis virus
                  (subtype Western, strain Neudoerfl)
INCLUDES        capsid protein C\ membrane protein M\ envelope
                  protein E\ nonstructural protein NS1\
                  nonstructural protein NS2a\ nonstructural protein
                  NS2b\ nonstructural protein NS3\ nonstructural
                  protein NS4a\ nonstructural protein NS4b\
                  nonstructural protein NS5
DATE            31-Dec-1989 #Sequence 30-Jun-1991 #Text 30-Sep-1992
PLACEMENT       2169.0    4.0    1.0    2.0    1.0
SOURCE          tick-borne encephalitis virus
ACCESSION       A31052\ A32596
REFERENCE
   #Authors     Mandl C.W., Heinz F.X., Kunz C.
   #Journal     Virology (1988) 166:197-205
   #Title       Sequence of the structural proteins of tick-borne
                  encephalitis virus (Western subtype) and
                  comparative analysis with other flaviviruses.
   #Reference-number A31052
   #Accession   A31052
   #Molecule-type genomic RNA
   #Residues    1-779 <MAN1>
REFERENCE
   #Authors     Mandl C.W., Heinz F.X., Stoeckl E., Kunz C.
   #Journal     Virology (1989) 173:291-301
```

```
   TITLE       Genome sequence of tick-borne encephalitis virus
                 (Western subtype) and comparative analysis of
                 nonstructural proteins with other flaviviruses.
   #Reference-number A32596
   #Accession   A32596
   #Molecule-type genomic RNA
   #Residues    767-3414 <MAN2>
COMMENT         This virus is a member of the family Flaviviridae.
SUPERFAMILY     #Name yellow fever virus genome polyprotein
KEYWORDS        capsid protein\ envelope protein\ glycoprotein\
                 membrane protein\ nonstructural protein\
                 polyprotein
FEATURE
   2-116                #Protein capsid protein C <CPC>\
   117-280              #Protein membrane protein M precursor
                          <MPP>\
   117-205              #Domain signal sequence <SIG>\
   206-280              #Protein membrane protein M <MPM>\
   246-264              #Domain transmembrane <TM1>\
   281-776              #Protein envelope protein E <EPE>\
   738-751              #Domain transmembrane <TM2>\
   777-1128             #Protein nonstructural protein NS1 <NS1>\
   1129-1358            #Protein nonstructural protein NS2a
                          <N2A>\
   1359-1489            #Protein nonstructural protein NS2b
                          <N2B>\
   1490-2110            #Protein nonstructural protein NS3 <NS3>\
   2111-2259            #Protein nonstructural protein NS4a
                          <N4A>\
   2260-2511            #Protein nonstructural protein NS4b
                          <N4B>\
   2512-3414            #Protein nonstructural protein NS5 <NS5>\
   144,434,641,753,861,
   983,999,1649,1988,
   2044,2447,2529,2686,
   2726                 #Binding-site carbohydrate (Asn)
                          (covalent) (predicted)
SUMMARY      #Molecular-weight 378383  #Length 3414  #Checksum  1083
SEQUENCE
COMMENT          Retrieved by alexk on Thu 25 Feb 93 10:21:17-PST using FastDB

Initial Score     =      6  Optimized Score  =      6  Significance =  3.09
Residue Identity  =   100%  Matches          =      6  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    RRVTTASAAQRRGRVGRQDGRTDEYIYSGQCDDDDSGLVQWKEAQILLDNITTLRGPVATFYGPEQDKMPEV
 1940       1950       1960       1970       1980       1990       2000       2010

                                  X     X
                                  WHVAAN
                                  ||||||
    AGHFRLTEEKRKHFRHLLTHCDFTPWLAWHVAANVSSVTDRSWTWEGPDRDAVDEASGDLVTFRSPNGAERT
          2020       2030       2040    X  2050       2060       2070       2080

    LRPVWKDARMFKEGRDIKEFVAYASGRRSFGDVLTGMSGVPELLRHRCVSALDVFYTLMHEE
        2090       2100       2110       2120       2130       2140


2. CELSA-1 (1-6)
   POLG_TBEVW   GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CO

 ID   POLG_TBEVW     STANDARD;      PRT;  3414 AA.
 AC   P14336;
 DT   01-JAN-1990 (REL. 13, CREATED)
 DT   01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
```

```
DE   GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE   PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE   PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
DE   RNA POLYMERASE (EC 2.7.7.48) (NS5)).
OS   TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE) (TBEV).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE.
RN   [1]
RP   SEQUENCE OF 1-779 FROM N.A.
RC   STRAIN=NEUDOERFL;
RM   88322870
RA   MANDL C.W., HEINZ F.X., KUNZ C.;
RL   VIROLOGY 166:197-205(1988).
RN   [2]
RP   SEQUENCE OF 767-3414 FROM N.A.
RC   STRAIN=NEUDOERFL;
RM   90051080
RA   MANDL C.W., HEINZ F.X., STOECKL E., KUNZ C.;
RL   VIROLOGY 173:291-301(1989).
CC   -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC       HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC       NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC   -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC       LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC       PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC       PROTEIN C AND MRNA.
DR   EMBL; M21498; TOGTBESP.
DR   EMBL; M33668; TBEGNE.
DR   PIR; A31052; GNWVNE.
KW   POLYPROTEIN; GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN;
KW   COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE;
KW   NONSTRUCTURAL PROTEIN.
FT   INIT_MET      1      1        REMOVED FROM CAPSID PROTEIN C BY THE
FT                                 CELLULAR AMINOPEPTIDASE.
FT   CHAIN         2    112        CAPSID PROTEIN C.
FT   PROPEP      113    205
FT   CHAIN       206    280        ENVELOPE GLYCOPROTEIN M.
FT   CHAIN       281    776        MAJOR ENVELOPE PROTEIN E.
FT   CHAIN       777   1128        NONSTRUCTURAL PROTEIN NS1.
FT   CHAIN      1129   1358        NONSTRUCTURAL PROTEIN NS2A.
FT   CHAIN      1359   1489        NONSTRUCTURAL PROTEIN NS2B.
FT   CHAIN      1490   2110        HELICASE (NS3).
FT   CHAIN      2111   2259        NONSTRUCTURAL PROTEIN NS4A.
FT   CHAIN      2260   2511        NONSTRUCTURAL PROTEIN NS4B.
FT   CHAIN      2512   3414        RNA-DIRECTED RNA POLYMERASE (NS5).
FT   TRANSMEM    101    112        HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL).
FT   TRANSMEM    247    259        POTENTIAL.
FT   TRANSMEM    266    280        POTENTIAL.
FT   TRANSMEM    738    751        POTENTIAL.
FT   CARBOHYD    144    144        POTENTIAL.
FT   CARBOHYD    434    434        POTENTIAL.
FT   CARBOHYD    861    861        POTENTIAL.
FT   CARBOHYD    983    983        POTENTIAL.
FT   CARBOHYD    999    999        POTENTIAL.
FT   CARBOHYD   2447   2447        POTENTIAL.
SQ   SEQUENCE   3414 AA;  378379 MW;  2.052432E+07 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:21:16-PST using FastDB

Initial Score     =      6  Optimized Score  =      6  Significance =  3.09
Residue Identity  =   100%  Matches          =      6  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    RRVTTASAAQRRGRVGRQDGRTDEYIYSGQCDDDDSGLVQWKEAQILLDNITTLRGPVATFYGPEQDKMPEV
 1940      1950      1960      1970      1980      1990      2000      2010

                                X     X
```

```
                                    | | | | | |
   AGHFRLTEEKRKHFRHLLTHCDFTPWLAWHVAANVSSVTDRSWTWEGPDRDAVDEASGDLVTFRSPNGAERT
         2020       2030       2040    X  2050       2060       2070       2080

   LRPVWKDARMFKEGRDIKEFVAYASGRRSFGDVLTGMSGVPELLRHRCVSALDVFYTLMHEE
       2090       2100       2110       2120       2130       2140
```

3. CELSA-1 (1-6)
   GNWVTB Genome polyprotein - Tick-borne encephalitis virus

```
ENTRY           GNWVTB     #Type Protein
TITLE           Genome polyprotein - Tick-borne encephalitis virus
                  (strain Sofjin)
INCLUDES        capsid protein C\ envelope protein prM\ envelope
                  protein M\ major envelope protein E\ nonstructural
                  protein NS1\ nonstructural protein NS2a\
                  nonstructural protein NS2b\ nonstructural protein
                  NS3\ nonstructural protein NS4a\ nonstructural
                  protein NS4b\ nonstructural protein NS5
DATE            31-Mar-1991 #Sequence 31-Mar-1991 #Text 30-Jun-1992
PLACEMENT       2169.0    4.0    1.0    1.0    1.0
SOURCE          tick-borne encephalitis virus
ACCESSION       A33776\ S06414
REFERENCE
   #Authors     Pletnev A.G., Yamshchikov V.F., Blinov V.M.
   #Journal     Virology (1990) 174:250-263
   #Title       Nucleotide sequence of the genome and complete amino
                  acid sequence of the polyprotein of tick-borne
                  encephalitis virus.
   #Reference-number A33776
   #Accession   A33776
   #Molecule-type genomic RNA
   #Residues    1-3412 <PLE>
   #Cross-reference GB:X07755
COMMENT         This virus is a member of the family Flaviviridae.
SUPERFAMILY     #Name yellow fever virus genome polyprotein
KEYWORDS        capsid protein\ envelope protein\ glycoprotein\
                  nonstructural protein\ polyprotein
FEATURE
   2-112                  #Protein capsid protein C <CPC>\
   113-205                #Protein envelope protein prM <PRM>\
   206-280                #Protein envelope protein M <PMM>\
   281-776                #Protein major envelope protein E <PPE>\
   777-1190               #Protein nonstructural protein NS1 <NS1>\
   1191-1358              #Protein nonstructural protein NS2a
                            <N2A>\
   1359-1489              #Protein nonstructural protein NS2b
                            <N2B>\
   1490-2110              #Protein nonstructural protein NS3 <NS3>\
   2111-2259              #Protein nonstructural protein NS4a
                            <N4A>\
   2260-2510              #Protein nonstructural protein NS4b
                            <N4B>\
   2511-3412              #Protein nonstructural protein NS5 <NS5>\
   144,434,641,753,861,
   983,999,1228,1649,
   1988,2044,2052,2447,
   2466,2685,2725         #Binding-site carbohydrate (Asn)
                            (covalent) (predicted)
SUMMARY     #Molecular-weight 377979  #Length 3412  #Checksum  7007
SEQUENCE
COMMENT         Retrieved by alexk on Thu 25 Feb 93 10:21:17-PST using FastDB
```

Initial Score = 6 Optimized Score = 6 Significance = 3.09

```
   RRVTTASAAQRRGRVGRQEGRTDEYIYSGQCDDDDSGLVQWKEAQILLDNITTLRGPVATFYGPEQDKMPEV
1940       1950       1960       1970       1980       1990       2000       2010

                                    X     X
                                    WHVAAN
                                    ||||||
   AGHFRLTEEKRKHFRHLLTHCDFTPWLAWHVAANVSSVTSRNWTWEGPEENTVDEANGDLVTFRSPNGAERT
         2020       2030       2040    X  2050       2060       2070       2080

   LRPVWRDARMFREGRDIREFVAYASGRRSFGDVLSGMSGVPELLRHRCVSAMDVFYTLMHEE
       2090       2100       2110       2120       2130       2140
```

4. CELSA-1 (1-6)
   POLG_TBEVS GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CO

```
ID   POLG_TBEVS     STANDARD;      PRT;  3412 AA.
AC   P07720; P07721;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE   PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE   PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
DE   RNA POLYMERASE (EC 2.7.7.48) (NS5)).
OS   TICK-BORNE ENCEPHALITIS VIRUS (STRAIN SOFJIN) (TBEV).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90101381
RA   PLETNEV A.G., YAMSHCHIKOV V.F., BLINOV V.M.;
RL   VIROLOGY 174:250-263(1990).
RN   [2]
RP   SEQUENCE OF 1-1190 FROM N.A.
RM   88319988
RA   YAMSHCHIKOV V.F., PLETNEV A.G.;
RL   NUCLEIC ACIDS RES. 16:7750-7750(1988).
RN   [3]
RP   SEQUENCE OF 1-683 AND 758-1002 FROM N.A.
RM   86220766
RA   PLETNEV A.G., YAMSHCHIKOV V.F., BLINOV V.M.;
RL   FEBS LETT. 200:317-321(1986).
CC   -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC       HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC       NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC   -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC       LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC       PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC       PROTEIN C AND MRNA.
CC   -!- THE NONSTRUCTURAL PROTEINS NS1 PRESENTS TWO ALTERNATIVE CLEAVAGE
CC       SITES FOR ITS C-TERMINUS, WHICH MAY DEFINE A SOLUBLE OR A
CC       MEMBRANE-BOUND FORM OF NS1.
DR   EMBL; X07755; TBEV1.
DR   EMBL; X03870; TOTBEV1.
DR   EMBL; X03871; TOTBEV2.
DR   PIR; A33776; GNWVTB.
DR   PIR; A24055; GNWVTE.
DR   PIR; B24055; MNWVTE.
KW   POLYPROTEIN; GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN;
KW   COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE;
KW   NONSTRUCTURAL PROTEIN.
FT   INIT_MET       1       1       REMOVED FROM CAPSID PROTEIN C BY THE
FT                                  CELLULAR AMINOPEPTIDASE.
FT   CHAIN          -       ---     CAPSID PROTEIN C
```

```
FT   PROPEP        115      205
FT   CHAIN         206      280        ENVELOPE GLYCOPROTEIN M.
FT   CHAIN         281      776        MAJOR ENVELOPE PROTEIN E.
FT   CHAIN         777    ?1128        NONSTRUCTURAL PROTEIN NS1 (OR 1190).
FT   CHAIN       ?1129     1358        NONSTRUCTURAL PROTEIN NS2A (OR 1191).
FT   CHAIN        1359     1489        NONSTRUCTURAL PROTEIN NS2B.
FT   CHAIN        1490     2110        HELICASE (NS3).
FT   CHAIN        2111     2259        NONSTRUCTURAL PROTEIN NS4A.
FT   CHAIN        2260     2510        NONSTRUCTURAL PROTEIN NS4B.
FT   CHAIN        2511     3412        RNA-DIRECTED RNA POLYMERASE (NS5).
FT   TRANSMEM      101      112        HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL).
FT   TRANSMEM      247      259        POTENTIAL.
FT   TRANSMEM      266      280        POTENTIAL.
FT   TRANSMEM      738      751        POTENTIAL.
FT   CARBOHYD      144      144        POTENTIAL.
FT   CARBOHYD      434      434
FT   CARBOHYD      861      861        POTENTIAL.
FT   CARBOHYD      983      983        POTENTIAL.
FT   CARBOHYD      999      999        POTENTIAL.
FT   CARBOHYD     1228     1228        POTENTIAL.
FT   CARBOHYD     2447     2447        POTENTIAL.
FT   CARBOHYD     2466     2466        POTENTIAL.
FT   CONFLICT      381      381        W -> S (IN REF. 3).
FT   CONFLICT      850      850        E -> D (IN REF. 3).
SQ   SEQUENCE   3412 AA;  377976 MW;  2.068228E+07 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:21:17-PST using FastDB

Initial Score     =      6  Optimized Score  =      6  Significance =  3.09
Residue Identity  =   100%  Matches          =      6  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    RRVTTASAAQRRGRVGRQEGRTDEYIYSGQCDDDDSGLVQWKEAQILLDNITTLRGPVATFYGPEQDKMPEV
1940      1950      1960      1970      1980      1990      2000      2010

                                  X     X
                                  WHVAAN
                                  ||||||
    AGHFRLTEEKRKHFRHLLTHCDFTPWLAWHVAANVSSVTSRNWTWEGPEENTVDEANGDLVTFRSPNGAERT
          2020      2030      2040    X 2050      2060      2070      2080

    LRPVWRDARMFREGRDIREFVAYASGRRSFGDVLSGMSGVPELLRHRCVSAMDVFYTLMHEE
        2090      2100      2110      2120      2130      2140
```

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O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-13-align.res made by alexk on Thu 25 Feb 93 10:47:27-PST.


Query sequence being compared:      CELSA-13 (1-5)
Number of sequences searched:                  50
Number of scores above cutoff:                 50

      Results of the initial comparison of CELSA-13 (1-5) with:
        File : celsa-13.pep

    100-
      -
N     -
U   50-
M     -                                                  *
B     -
E     -
R     -
      -
O     -                                                                 *
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -
S     0-------------------------------------------------------------------
       ||     |     ||      |    | |      |   | |      |      |      |
SCORE 0|     1     |1      2    | 2      3   | 3      4      4      5
STDEV -7          -5           -2            0


                          PARAMETERS

Similarity matrix      Unitary     K-tuple                    2
Mismatch penalty             5     Joining penalty           20
Gap penalty               1.00     Window size                5
Gap size penalty          0.26
Cutoff score                 0
Randomization group          0

                       SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                              4             5                    0.42

Times:                      CPU                      Total Elapsed
                    00:00:00.02                      00:00:01.00

Number of residues:                      15270
Number of sequences searched:               50
Number of scores above cutoff:              50
```

Significance is calculated based on initial score.

11 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. A37113	*Ryanodine receptor, cardiac	4969	5	5	2.39	0
2. BVFFSL	sol protein, large splice for	1597	5	5	2.39	0
3. SOL_DROME	SMALL OPTIC LOBES PROTEIN.	1597	5	5	2.39	0
4. A31854	Cytochrome P450 51 lanosterol	528	5	5	2.39	0
5. CP51_CANTR	CYTOCHROME P450 L1 (P450-L1A1	528	5	5	2.39	0
6. STP1_ARATH	GLUCOSE TRANSPORTER (SUGAR CA	522	5	5	2.39	0
7. S14627	*Glucose transport protein -	522	5	5	2.39	0
8. S12042	*Sugar transport protein STP1	522	5	5	2.39	0
9. B35901	*Calcium channel alpha-1 chai	164	5	5	2.39	0
10. J00700	Hypothetical 11K protein (mmo	103	5	5	2.39	0
11. YMMO_METCA	HYPOTHETICAL 11.9 KD PROTEIN	103	5	5	2.39	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
12. C24735	Glutathione transferase, 2-2	9	4	4	0.00	0
13. B24735	Glutathione transferase, 1-2	18	4	4	0.00	0
14. D24735	Glutathione transferase, 2-2	19	4	4	0.00	0
15. A24735	Glutathione transferase, 1-1	26	4	4	0.00	0
16. S21278	*Glutathione transferase chai	28	4	4	0.00	0
17. S09585	*Glutathione transferase - Ra	31	4	4	0.00	0
18. S03358	*Glutathione transferase - Ra	31	4	4	0.00	0
19. J00099	Hypothetical 7K protein - Pap	68	4	4	0.00	0
20. V07K_PMV	7 KD PROTEIN (ORF 4).	68	4	4	0.00	0

1. CELSA-13 (1-5)
   A37113 *Ryanodine receptor, cardiac muscle - Rabbit

```
ENTRY           A37113     #Type Protein
TITLE           *Ryanodine receptor, cardiac muscle - Rabbit
DATE            12-Feb-1991 #Sequence 12-Feb-1991 #Text 12-Feb-1991
PLACEMENT          0.0    0.0    0.0    0.0    0.0
COMMENT         *This entry is not verified.
SOURCE          Oryctolagus cuniculus #Common-name domestic rabbit
REFERENCE
   #Authors     Otsu K., Willard H.F., Khanna V.K., Zorzato F.,
                  Green N.M., MacLennan D.H.
   #Journal     J. Biol. Chem. (1990) 265:13472-13483
   #Title       Molecular cloning of cDNA encoding the Ca(2+)
                  release channel (ryanodine receptor) of rabbit
                  cardiac muscle sarcoplasmic reticulum.
   #Reference-number A37113
   #Accession   A37113
SUMMARY     #Molecular-weight 565069  #Length 4969  #Checksum  5421
SEQUENCE
COMMENT         Retrieved by alexk on Thu 25 Feb 93 10:39:50-PST using FastDB

Initial Score     =      5  Optimized Score  =      5  Significance =  2.39
Residue Identity  =   100%  Matches          =      5  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    DLTSSDTFKEYDPDGKGIISKRDFHKAMESHKHYTQSETEFLLSCAETDENETLDYEEFVKRFHEPAKDIGF
     4030      4040      4050      4060      4070      4080      4090
```

```
                                  VLNYF
                                  |||||
   NVAVLLTNLSEHMPNDTRLQTFLELAESVLNYFQPFLGRIEIMGSAKRIERVYFEISESSRTQWEKPQVKES
  4100       4110       4120       4130       4140       4150       4160

   KRQFIFDVVNEGGEKEKMELFVNFCEDTIFEMQLAAQISESDLNERSANKEESEKERPEEQ
4170       4180       4190       4200       4210       4220       4230
```

2. CELSA-13 (1-5)
   BVFFSL sol protein, large splice form - Fruit fly

```
ENTRY            BVFFSL      #Type Protein
TITLE            sol protein, large splice form - Fruit fly
                   (Drosophila melanogaster)
DATE             30-Jun-1992 #Sequence 30-Jun-1992 #Text 30-Jun-1992
PLACEMENT        1221.0    1.0    1.0    1.0    1.0
SOURCE           Drosophila melanogaster
ACCESSION        A41146
REFERENCE
   #Authors      Delaney S.J., Hayward D.C., Barleben F., Fischbach
                   K.F., Miklos G.L.G.
   #Journal      Proc. Natl. Acad. Sci. U.S.A. (1991) 88:7214-7218
   #Title        Molecular cloning and analysis of small optic lobes,
                   a structural brain gene of Drosophila
                   melanogaster.
   #Reference-number A41146
   #Accession    A41146
   #Molecule-type mRNA
   #Residues     1-1597 <DEL>
   #Cross-reference GB:M64084
COMMENT          The sol (small optic lobes) mutation eliminates
                   certain classes of columnar neurons.
COMMENT          An alternate splice form of 395 amino acids is
                   observed, in which the first 393 are identical to
                   the large sol protein.
GENETIC
   #Segment-number 19F4
   #Name           sol
SUPERFAMILY      #Name sol protein
FEATURE
   1017-1320              #Domain calpain catalytic domain homology
                            <CAL>\
   10-29                  #Region zinc finger-like motif <ZN1>\
   139-158                #Region zinc finger-like motif\
   647-667                #Region zinc finger-like motif\
   711-730                #Region zinc finger-like motif\
   752-771                #Region zinc finger-like motif\
   934-953                #Region zinc finger-like motif\
   1082                   #Active-site Cys (predicted)\
   1248                   #Active-site His (predicted)\
   1268                   #Active-site Asn (predicted)
SUMMARY      #Molecular-weight 174713  #Length 1597  #Checksum  8253
SEQUENCE
COMMENT          Retrieved by alexk on Thu 25 Feb 93 10:39:51-PST using FastDB
```

```
Initial Score     =      5  Optimized Score  =      5  Significance =  2.39
Residue Identity  =   100%  Matches          =      5  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0
```

```
   AQLLSSRCVRFLMGASCGGGNMKVDEEEYQQKGLRPRHAYSVLDVKDIQGHRLLKLRNPWGHYSWRGDWSDD
       1220       1230       1240       1250       1260       1270       1280

                                  X   X
                                  VLNYF
                                  |||||
```

```
----------------------------------------------------------------------SSLWTDDLRDALMPHGASEGVFWISFEDVLNYFDCIDICKVRSGWNEVRLQGTLQPLCSISCVLLTVLEPTE
    1290        1300        1310     X 1320        1330        1340        1350

AEFTLFQEGQRNSEKSQRSQLDLCVVIFRTRSPAAPEIGRLVEHSKRQVRGFVGCHKMLER
    1360        1370        1380        1390        1400        1410
```

3. CELSA-13 (1-5)
SOL_DROME SMALL OPTIC LOBES PROTEIN.

```
ID   SOL_DROME      STANDARD;      PRT;  1597 AA.
AC   P27398;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   SMALL OPTIC LOBES PROTEIN.
GN   SOL.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RM   91334436
RA   DELANEY S.J., HAYWARD D.C., BARLEBEN F., FISCHBACH K.F.,
RA   MIKLOS G.L.G.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:7214-7218(1991).
CC   -!- THE SOL (SMALL OPTIC LOBES) MUTATION ELIMINATES CERTAIN CLASSES OF
CC       COLUMNAR NEURONS.
CC   -!- ALTERNATIVE SPLICING: AN ALTERNATE SPLICE FORM OF 395 AMINO ACIDS
CC       IS OBSERVED, IN WHICH THE FIRST 393 ARE IDENTICAL TO THE LARGE SOL
CC       PROTEIN.
CC   -!- SIMILARITY: TO CALPAINS EUKARYOTIC THIOL PROTEASES.
DR   EMBL; M64084; DMSOL.
DR   PIR; A41146; BVFFSL.
DR   FLYBASE; 03464; RELEASE 9206.
KW   ALTERNATIVE SPLICING; ZINC-FINGER; HYDROLASE; THIOL PROTEASE.
FT   ZN_FING       10     29       C4-TYPE.
FT   ZN_FING      139    158       C4-TYPE.
FT   ZN_FING      647    667       C4-TYPE.
FT   DOMAIN       673    689       GLN-RICH.
FT   DOMAIN       690    697       POLY-HIS.
FT   ZN_FING      711    730       C4-TYPE.
FT   ZN_FING      752    771       C4-TYPE.
FT   ZN_FING      934    953       C4-TYPE.
FT   DOMAIN      1017   1320       CALPAIN CATALYTIC DOMAIN.
FT   ACT_SITE    1082   1082       BY SIMILARITY.
FT   ACT_SITE    1248   1248       BY SIMILARITY.
FT   ACT_SITE    1268   1268       BY SIMILARITY.
SQ   SEQUENCE   1597 AA;  174714 MW;  1.268343E+07 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:39:51-PST using FastDB

Initial Score    =      5  Optimized Score  =      5  Significance =  2.39
Residue Identity =   100%  Matches          =      5  Mismatches   =     0
Gaps             =      0  Conservative Substitutions              =     0

AQLLSSRCVRFLMGASCGGGNMKVDEEEYQQKGLRPRHAYSVLDVKDIQGHRLLKLRNPWGHYSWRGDWSDD
    1220        1230        1240        1250        1260        1270        1280

                                    X   X
                                    VLNYF
                                    |||||
SSLWTDDLRDALMPHGASEGVFWISFEDVLNYFDCIDICKVRSGWNEVRLQGTLQPLCSISCVLLTVLEPTE
    1290.       1300        1310     X 1320        1330        1340        1350

AEFTLFQEGQRNSEKSQRSQLDLCVVIFRTRSPAAPEIGRLVEHSKRQVRGFVGCHKMLER
```

4. CELSA-13 (1-5)
A31854 Cytochrome P450 51 lanosterol 14alpha-demethylase

```
ENTRY            A31854      #Type Protein
TITLE            Cytochrome P450 51 lanosterol 14alpha-demethylase -
                   Imperfect fungus (Candida tropicalis)
ALTERNATE-NAME   cytochrome P450 14DM
DATE             07-Jun-1990 #Sequence 07-Jun-1990 #Text 10-Aug-1992
PLACEMENT           0.0     0.0     0.0     0.0     0.0
SOURCE           Candida tropicalis
ACCESSION        A31854
REFERENCE
   #Authors      Chen C., Kalb V.F., Turi T.G., Loper J.C.
   #Journal      DNA (1988) 7:617-626
   #Title        Primary structure of the cytochrome P450 lanosterol
                   14alpha-demethylase gene from Candida tropicalis.
   #Reference-number A31854
   #Accession    A31854
   #Molecule-type DNA
   #Residues     1-528 <CHE>
SUPERFAMILY      #Name cytochrome P450
KEYWORDS         heme\ monooxygenase\ oxidoreductase
FEATURE
   470                      #Binding-site heme iron (Cys) (axial
                              ligand)
SUMMARY       #Molecular-weight 60927  #Length 528  #Checksum  4431
SEQUENCE
COMMENT          Retrieved by alexk on Thu 25 Feb 93 10:39:51-PST using FastDB

Initial Score     =      5  Optimized Score  =      5  Significance =  2.39
Residue Identity  =   100%  Matches          =      5  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    M@PYEFFEKCRLKYGDVFSFMLLGKVMTVYLGPKGHEFIYNAKLSDVSAEEAYTHLTTPVFGKGVIYDCPNS
       70        80        90       100       110       120       130

                                  X   X
                                  VLNYF
                                  |||||
    RLMEQKKFAKFALTTDSFKTYVPKIREEVLNYFVNDVSFKTKERDHGVASVMKTQPEITIFTASRCLFGDEM
    140       150       160      X 170       180       190       200

    RKSFDRSFA@LYADLDKGFTPINFVFPNLPLPHYWRRDAAQRKISAHYMKEIKRRRESGDI
  210       220       230       240       250       260       270
```

5. CELSA-13 (1-5)
CP51_CANTR CYTOCHROME P450 L1 (P450-L1A1) (LANOSTEROL 14-ALPH

```
ID   CP51_CANTR     STANDARD;      PRT;   528 AA.
AC   P14263;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE   CYTOCHROME P450 L1 (P450-L1A1) (LANOSTEROL 14-ALPHA DEMETHYLASE)
DE   (EC 1.14.14.1).
GN   CYP51 OR 14DM.
OS   CANDIDA TROPICALIS (YEAST).
OC   EUKARYOTA; FUNGI; DEUTEROMYCOTINA (IMPERFECT FUNGI).
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89152749
RA   CHEN C., KALB V.F., TURI T.G., LOPER J.C.;
```

```
RP   SEQUENCE OF 434-528 FROM N.A.
RM   87298576
RA   CHEN C., TURI T.G., SANGLARD D., LOPER J.C.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 146:1311-1317(1987).
CC   -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC       MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC       COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC   -!- CATALYTIC ACTIVITY: 14-ALPHA-DEMETHYLATION OF LANOSTEROL.
DR   EMBL; M23673; M23673.
DR   EMBL; M17595; CT14DM.
DR   PIR; A31854; A31854.
DR   PIR; A26828; A26828.
DR   PROSITE; PS00086; CYTOCHROME_P450.
KW   ELECTRON TRANSPORT; OXIDOREDUCTASE; MONOOXYGENASE; MEMBRANE;
KW   HEME.
FT   BINDING     470    470       HEME.
SQ   SEQUENCE   528 AA;  60928 MW;  1513726 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:39:51-PST using FastDB
```

```
Initial Score     =       5  Optimized Score  =       5  Significance =  2.39
Residue Identity  =    100%  Matches          =       5  Mismatches   =     0
Gaps              =       0  Conservative Substitutions               =     0

    MQPYEFFEKCRLKYGDVFSFMLLGKVMTVYLGPKGHEFIYNAKLSDVSAEEAYTHLTTPVFGKGVIYDCPNS
       70        80        90       100       110       120       130

                                  X   X
                                  VLNYF
                                  |||||
    RLMEQKKFAKFALTTDSFKTYVPKIREEVLNYFVNDVSFKTKERDHGVASVMKTQPEITIFTASRCLFGDEM
    140       150       160      X 170       180       190       200

    RKSFDRSFAQLYADLDKGFTPINFVFPNLPLPHYWRRDAAQRKISAHYMKEIKRRRESGDI
  210       220       230       240       250       260       270
```

6. CELSA-13 (1-5)
   STP1_ARATH GLUCOSE TRANSPORTER (SUGAR CARRIER).

```
ID   STP1_ARATH     STANDARD;      PRT;   522 AA.
AC   P23586;
DT   01-NOV-1991 (REL. 20, CREATED)
DT   01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT   01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
DE   GLUCOSE TRANSPORTER (SUGAR CARRIER).
GN   STP1.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC   CAPPARALES; CRUCIFERAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. LANDSBERG ERECTA;
RM   91005995
RA   SAUER N., FRIEDLAENDER K., GRAEML-WICKE U.;
RL   EMBO J. 9:3045-3050(1990).
CC   -!- FUNCTION: ACTIVE UPTAKE OF HEXOSES. PROBABLE GLUCOSE/HYDROGEN
CC       SYMPORT.
CC   -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC SUGAR SYMPORTERS.
DR   EMBL; X55350; ATSTP1.
DR   PIR; S12042; S12042.
DR   PIR; S14627; S14627.
DR   PROSITE; PS00216; SUGAR_TRANSPORT_1.
DR   PROSITE; PS00217; SUGAR_TRANSPORT_2.
KW   DUPLICATION; TRANSMEMBRANE; SUGAR TRANSPORT; SYMPORT.
FT   TRANSMEM      ...      POTENTIAL.
```

```
FT   TRANSMEM      84      104         POTENTIAL.
FT   TRANSMEM     113      133         POTENTIAL.
FT   TRANSMEM     141      161         POTENTIAL.
FT   TRANSMEM     168      188         POTENTIAL.
FT   TRANSMEM     200      220         POTENTIAL.
FT   TRANSMEM     285      305         POTENTIAL.
FT   TRANSMEM     321      341         POTENTIAL.
FT   TRANSMEM     349      369         POTENTIAL.
FT   TRANSMEM     385      405         POTENTIAL.
FT   TRANSMEM     424      444         POTENTIAL.
FT   TRANSMEM     453      473         POTENTIAL.
SQ   SEQUENCE   522 AA;  57596 MW;  1520081 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:39:51-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =  2.39
Residue Identity =    100%  Matches          =       5  Mismatches   =     0
Gaps              =       0  Conservative Substitutions               =     0

    SSLYLAALISSLVASTVTRKFGRRLSMLFGGILFCAGALINGFAKHVWMLIVGRILLGFGIGFANQAVPLYL
      90        100        110        120        130        140        150

                                    X    X
                                    VLNYF
                                    |||||
    SEMAPYKYRGALNIGFQLSITIGILVAEVLNYFFAKIKGGWGWRLSLGGAVVPALIITIGSLVLPDTPNSMI
   160        170        180        190        200        210        220        230

    ERGQHEEAKTKLRRIRGVDDVSQEFDDLVAASKESQSIEHPWRNLLRRKYRPHLTMAVMIP
           240        250        260        270        280        290


7. CELSA-13 (1-5)
   S14627        *Glucose transport protein - Arabidopsis thaliana

 ENTRY             S14627     #Type Protein
 TITLE             *Glucose transport protein - Arabidopsis thaliana
 DATE              28-Aug-1992 #Sequence 28-Aug-1992 #Text 28-Aug-1992
 PLACEMENT            0.0     0.0     0.0     0.0     0.0
 COMMENT           *This entry is not verified.
 SOURCE            Arabidopsis thaliana #Common-name mouse-ear cress
 REFERENCE
    #Authors       Sauer N., Friedl K., Wicke U.
    #Citation      submitted to the EMBL Data Library, October 1990
    #Title         Primary structure, genomic organization &
                     heterologous expression of a glucose transporter
                     from Arabidopsis thaliana.
    #Reference-number S14627
    #Accession    S14627
    #Cross-reference EMBL:X55350
 SUMMARY         #Molecular-weight 57596  #Length 522  #Checksum  5679
 SEQUENCE
 COMMENT           Retrieved by alexk on Thu 25 Feb 93 10:39:51-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =  2.39
Residue Identity =    100%  Matches          =       5  Mismatches   =     0
Gaps              =       0  Conservative Substitutions               =     0

    SSLYLAALISSLVASTVTRKFGRRLSMLFGGILFCAGALINGFAKHVWMLIVGRILLGFGIGFANQAVPLYL
      90        100        110        120        130        140        150

                                    X    X
                                    VLNYF
                                    |||||
    SEMAPYKYRGALNIGFQLSITIGILVAEVLNYFFAKIKGGWGWRLSLGGAVVPALIITIGSLVLPDTPNSMI
   160        170        180        190        200        210        220        230
```

```
                   ERGQHEEAKTKLRRIRGVDDVSQEFDDLVAASKESQSIEHPWRNLLRRKYRPHLTMAVMIP
          240         250         260         270         280         290
```

8\. CELSA-13 (1-5)
S12042 *Sugar transport protein STP1 - Arabidopsis thalia

```
 ENTRY           S12042     #Type Protein
 TITLE           *Sugar transport protein STP1 - Arabidopsis thaliana
 DATE            26-Sep-1992 #Sequence 26-Sep-1992 #Text 26-Sep-1992
 PLACEMENT          0.0     0.0     0.0     0.0     0.0
 COMMENT         *This entry is not verified.
 SOURCE          Arabidopsis thaliana #Common-name mouse-ear cress
 REFERENCE
    #Authors     Sauer N., Friedlaender K., Graeml-Wicke U.
    #Journal     EMBO J. (1990) 9:3045-3050
    #Title       Primary structure, genomic organization and
                   heterologous expression of a glucose transporter
                   from Arabidopsis thaliana.
    #Reference-number S12042
    #Accession    S12042
    #Cross-reference EMBL:X55350
 SUMMARY        #Molecular-weight 57596  #Length 522  #Checksum  5679
 SEQUENCE
 COMMENT         Retrieved by alexk on Thu 25 Feb 93 10:39:51-PST using FastDB

Initial Score      =       5  Optimized Score   =       5  Significance =  2.39
Residue Identity =    100%  Matches           =       5  Mismatches   =      0
Gaps               =       0  Conservative Substitutions                 =      0

    SSLYLAALISSLVASTVTRKFGRRLSMLFGGILFCAGALINGFAKHVWMLIVGRILLGFGIGFANQAVPLYL
      90        100        110        120        130        140        150

                                     X   X
                                     VLNYF
                                     |||||
   SEMAPYKYRGALNIGFQLSITIGILVAEVLNYFFAKIKGGWGWRLSLGGAVVPALIITIGSLVLPDTPNSMI
  160        170        180        190        200        210        220        230

   ERGQHEEAKTKLRRIRGVDDVSQEFDDLVAASKESQSIEHPWRNLLRRKYRPHLTMAVMIP
         240        250        260        270        280        290
```

9\. CELSA-13 (1-5)
B35901 *Calcium channel alpha-1 chain, dihydropyridine

```
 ENTRY           B35901     #Type Protein (fragment)
 TITLE           *Calcium channel alpha-1 chain, dihydropyridine
                   sensitive, homolog B, brain - Rat (fragment)
 DATE            18-Apr-1991 #Sequence 18-Apr-1991 #Text 18-Apr-1991
 PLACEMENT          0.0     0.0     0.0     0.0     0.0
 COMMENT         *This entry is not verified.
 SOURCE          Rattus norvegicus #Common-name Norway rat
 REFERENCE
    #Authors     Snutch T.P., Leonard J.P., Gilbert M.M., Lester
                   H.A., Davidson N.
    #Journal     Proc. Natl. Acad. Sci. U.S.A. (1990) 87:3391-3395
    #Title       Rat brain expresses a heterogeneous family of
                   calcium channels.
    #Reference-number A35901
    #Accession    B35901
 SUMMARY                                    #Length 164  #Checksum  2550
 SEQUENCE
 COMMENT         Retrieved by alexk on Thu 25 Feb 93 10:39:52-PST using FastDB
```

```
Residue Identity =   100%  Matches          =       5  Mismatches   =       0
Gaps             =       0  Conservative Substitutions               =       0

                   X    X
                   VLNYF
                   |||||
    FSLECILKIIAFGVLNYFRDAWDVFDFVTVLGSITDILVTEIANNFINLSFLRLFRAARLIKLLRQGYTIRI
            10    X    20         30         40         50         60         70

    LLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVFGNIALDDGTSIN
          80         90         100        110


10. CELSA-13 (1-5)
    JQ0700        Hypothetical 11K protein (mmoC 5' region) -

 ENTRY            JQ0700      #Type Protein
 TITLE            Hypothetical 11K protein (mmoC 5' region) -
                    Methylococcus capsulatus
 ALTERNATE-NAME   hypothetical protein Y
 DATE             31-Mar-1992 #Sequence 31-Mar-1992 #Text 31-Mar-1992
 PLACEMENT           0.0     0.0     0.0     0.0     0.0
 SOURCE           Methylococcus capsulatus
 ACCESSION        JQ0700
 REFERENCE
    #Authors      Stainthorpe A.C., Lees V., Salmond G.P.C., Dalton
                    H., Murrell J.C.
    #Journal      Gene (1990) 91:27-34
    #Title        The methane monooxygenase gene cluster of
                    Methylococcus capsulatus (Bath).
    #Reference-number JQ0700
    #Accession    JQ0700
    #Molecule-type DNA
    #Residues     1-103 <STA>
 SUMMARY        #Molecular-weight 11942  #Length 103  #Checksum  8171
 SEQUENCE
 COMMENT          Retrieved by alexk on Thu 25 Feb 93 10:39:52-PST using FastDB

Initial Score    =       5  Optimized Score  =       5  Significance =   2.39
Residue Identity =   100%  Matches          =       5  Mismatches   =       0
Gaps             =       0  Conservative Substitutions               =       0

    MVESAFQPFSGDADEWFEEPRPQAGFFPSADWHLLKRDETYAAYAKDLDFMWRWVIVREERIVQEGCSISLE
            10         20         30         40         50         60         70

            X    X
            VLNYF
            |||||
    SSIRAVTHVLNYFGMTEQRAPAEDRTGGVQH
          80    X    90         100


11. CELSA-13 (1-5)
    YMMO_METCA    HYPOTHETICAL 11.9 KD PROTEIN IN MMOZ-MMOC INTERGEN

 ID   YMMO_METCA      STANDARD;      PRT;   103 AA.
 AC   P22867;
 DT   01-AUG-1991 (REL. 19, CREATED)
 DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT   01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 11.9 KD PROTEIN IN MMOZ-MMOC INTERGENIC REGION (ORFY).
 OS   METHYLOCOCCUS CAPSULATUS.
 OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
 OC   METHYLOCOCCACEAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
```

RM 90382694
RA STAINTHORPE A.C., LEES V., SALMOND G.P.C., DALTON H., MURRELL J.C.;
RL GENE 91:27-34(1990).
DR EMBL; M58498; MCMMOA.
DR PIR; JQ0700; JQ0700.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 103 AA; 11942 MW; 52861 CN;
CC -!- Retrieved by alexk on Thu 25 Feb 93 10:39:52-PST using FastDB

Initial Score	=	5	Optimized Score	=	5	Significance = 2.39
Residue Identity	=	100%	Matches	=	5	Mismatches = 0
Gaps	=	0	Conservative Substitutions			= 0

```
    MVESAFQPFSGDADEWFEEPRPQAGFFPSADWHLLKRDETYAAYAKDLDFMWRWVIVREERIVQEGCSISLE
             10        20        30        40        50        60        70

             X   X
             VLNYF
             |||||
    SSIRAVTHVLNYFGMTEQRAPAEDRTGGVQH
           80    X   90        100
```

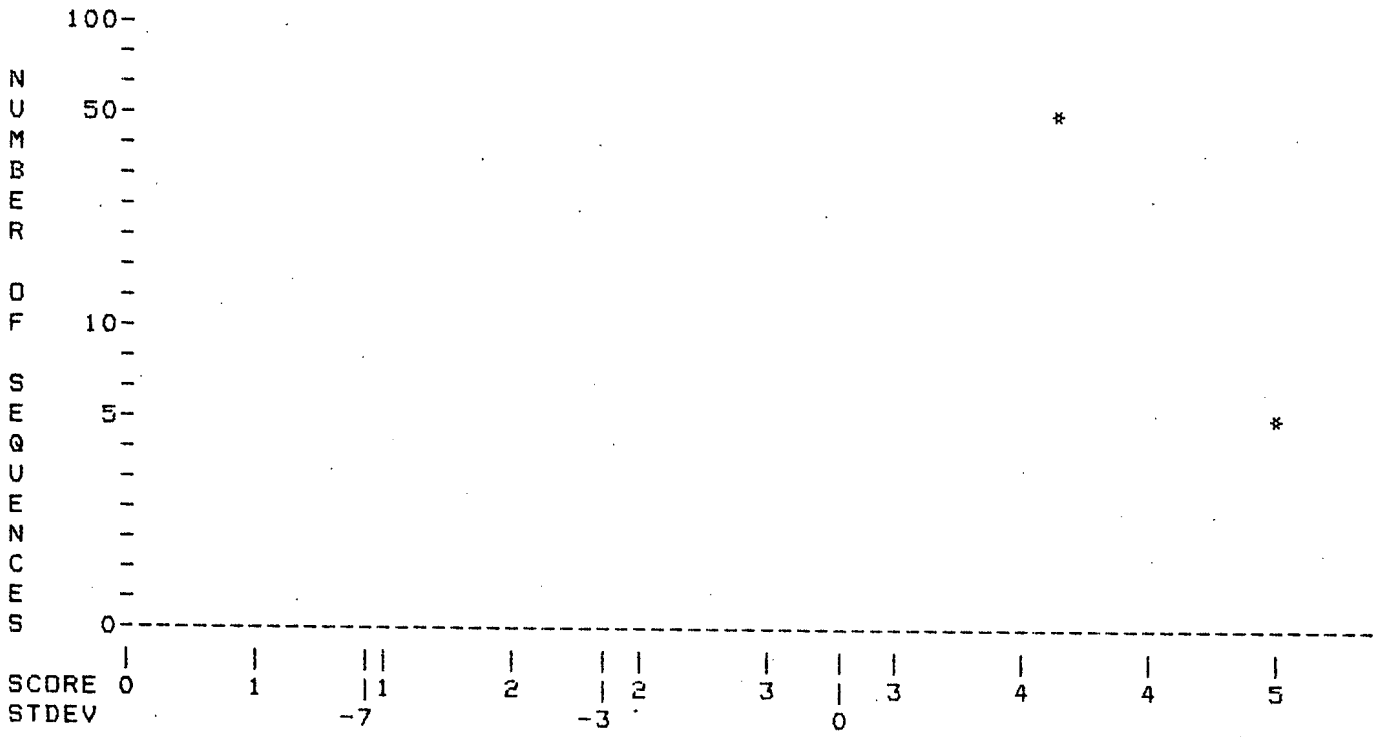
O| |O IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-3-align.res made by alexk on Thu 25 Feb 93 10:48:08-PST.

Query sequence being compared: CELSA-3 (1-5)
Number of sequences searched: 50
Number of scores above cutoff: 50

Results of the initial comparison of CELSA-3 (1-5) with:
File : celsa-3.pep



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	4	5	0.30

Times:	CPU	Total Elapsed
	00:00:00.01	00:00:00.00

Number of residues:	8896
Number of sequences searched:	50
Number of scores above cutoff:	50

-- -------- based on initial score.

5 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. P82507	Pullulanase protein.	1096	5	5	3.30	0
2. A26879	alpha-Dextrin endo-1,6-alpha-	1096	5	5	3.30	0
3. PULA_KLEAE	PULLULANASE (EC 3.2.1.41) (AL	1096	5	5	3.30	0
4. S12888	*DNA-binding protein II - The	95	5	5	3.30	0
5. DBH_THETH	DNA-BINDING PROTEIN II.	95	5	5	3.30	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
6. S10561	*Photosystem II 21K protein -	66	4	4	0.00	0
7. CCPS5S	Cytochrome c551 - Pseudomonas	82	4	4	0.00	0
8. C551_PSEST	CYTOCHROME C551.	82	4	4	0.00	0
9. CCPB6	Cytochrome c6 - Plectonema bo	85	4	4	0.00	0
10. CYC6_PLEBO	CYTOCHROME C6 (SOLUBLE CYTOCH	85	4	4	0.00	0
11. CCAI6	Cytochrome c6 - Anabaena vari	86	4	4	0.00	0
12. CYC6_ANAVA	CYTOCHROME C6 (SOLUBLE CYTOCH	86	4	4	0.00	0
13. DNBS2F	DNA-binding protein II - Baci	90	4	4	0.00	0
14. DBH_BACST	DNA-BINDING PROTEIN II (HB) (	90	4	4	0.00	0
15. S00015	DNA-binding protein HB - Baci	92	4	4	0.00	0
16. B39409	*DNA-binding protein HB - Bac	92	4	4	0.00	0
17. DBH_BACSU	DNA-BINDING PROTEIN II (HB) (	92	4	4	0.00	0
18. R05446	CAT-GLP-1 hybrid protein.	104	4	4	0.00	0
19. Q0ECRP	Hypothetical protein A-105 -	105	4	4	0.00	0
20. S06985	Hypothetical protein (nifH1 3	105	4	4	0.00	0

1. CELSA-3 (1-5)
   P82507 Pullulanase protein.

ID P82507 standard; protein; 1096 AA.
AC P82507;
DT 01-NOV-1990 (first entry)
DE Pullulanase protein.
KW Pullulanase; starch; alcohol prodn.
OS Klebsiella aerogenes.
PN J63245676-A.
PD 12-OCT-1988.
PF 31-MAR-1987; 078355.
PR 31-MAR-1987; JP-078355.
PA (ELED) Denki Kagaku Kogyo KK; (SUNR) Suntory Ltd.
DR WPI; 88-333488/47.
DR N-PSDB; N81341.
PT Gene encoding pullulanase - derived from recombinant plasmid pMP1 contg.
PT gene from Klebsiella genus.
PS Disclosure; p; Japanese.
CC The pullulanase protein cleaves alpha-1,6-glucoside bonds of starch and
CC is effective in decomposition of branched starch. It is used in the
CC prodn. of maltose and glucose from starch, and of alcohol from starch
CC via glucose. Amino acid residues 1-19 can be deleted.
SQ Sequence 1096 AA;
SQ 108 A; 63 R; 42 N; 93 D; 0 B; 10 C; 51 Q; 42 E; 0 Z; 89 G; 22 H;
SQ 38 I; 86 L; 42 K; 21 M; 31 F; 52 P; 96 S; 70 T; 18 W; 41 Y; 81 V;
CC Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 3.30

```
Gaps            =       0  Conservative Substitutions                =       0

    SFSDFTDRTVSVIAGNSAVYDSRADAFRAAFGVALADAHWVDKTTLLWPGGENKPIVRLYYSHSSKVAADSN
  160       170       180       190       200       210       220       230

                                  X   X
                                  YPAFK
                                  |||||
    GEFSDKYVKLTPTTVNQQVSMRFPHLASYPAFKLPDDVNVDELLQGDDGGIAESDGILSLSHPGADRRRAGR
        240       250       260   X   270       280       290       300

    YLCRRAEALSYGAQLTDSGVTFRVWAPTAQQVELVIYSADKKVIASHPMTRDSASGAWSWQ
        310       320       330       340       350       360


2. CELSA-3 (1-5)
   A26879        alpha-Dextrin endo-1,6-alpha-glucosidase precursor

 ENTRY            A26879      #Type Protein
 TITLE            alpha-Dextrin endo-1,6-alpha-glucosidase precursor -
                    Klebsiella pneumoniae #EC-number 3.2.1.41
 ALTERNATE-NAME   pullulanase
 DATE             30-Jun-1988 #Sequence 30-Jun-1988 #Text 31-Sep-1992
 PLACEMENT           0.0     0.0     0.0     0.0     0.0
 SOURCE           Klebsiella pneumoniae
 ACCESSION        A26879
 REFERENCE        (K. aerogenes, strain W70)
    #Authors      Katsuragi N., Takizawa N., Murooka Y.
    #Journal      J. Bacteriol. (1987) 169:2301-2306
    #Title        Entire nucleotide sequence of the pullulanase gene
                   of Klebsiella aerogenes W70.
    #Reference-number A26879
    #Accession    A26879
    #Molecule-type DNA
    #Residues     1-1096 <KAT>
 GENETIC
    #Name             pulA
 KEYWORDS         glycosidase\ hydrolase
 FEATURE
    1-19                      #Domain signal sequence <SIG>\
    20-1096                   #Protein alpha-dextrin endo-1,
                                6-alpha-glucosidase <MAT>
 SUMMARY      #Molecular-weight 119335  #Length 1096  #Checksum  1390
 SEQUENCE
 COMMENT          Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =  3.30
Residue Identity  =    100%  Matches          =       5  Mismatches   =       0
Gaps              =       0  Conservative Substitutions                =       0

    SFSDFTDRTVSVIAGNSAVYDSRADAFRAAFGVALADAHWVDKTTLLWPGGENKPIVRLYYSHSSKVAADSN
  160       170       180       190       200       210       220       230

                                  X   X
                                  YPAFK
                                  |||||
    GEFSDKYVKLTPTTVNQQVSMRFPHLASYPAFKLPDDVNVDELLQGDDGGIAESDGILSLSHPGADRRRAGR
        240       250       260   X   270       280       290       300

    YLCRRAEALSYGAQLTDSGVTFRVWAPTAQQVELVIYSADKKVIASHPMTRDSASGAWSWQ
        310       320       330       340       350       360


3. CELSA-3 (1-5)
   PULA_KLEAE   PULLULANASE (EC 3.2.1.41) (ALPHA-DEXTRIN ENDO-1,6-
```

```
ID   PULA_KLEAE     STANDARD;      PRT;  1096 AA.
AC   P07811;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT   01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE   PULLULANASE (EC 3.2.1.41) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)
DE   (PULLULAN 6-GLUCANOHYDROLASE).
GN   PULA.
OS   KLEBSIELLA AEROGENES.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=W70;
RM   87194626
RA   KATSURAGI N., TAKIZAWA N., MUROOKA Y.;
RL   J. BACTERIOL. 169:2301-2306(1987).
CC   -!- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES
CC       (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO
CC       FORM MALTOTRIOSE.
CC   -!- SUBUNIT: HOMOTRIMER.
DR   EMBL; M16187; KAPULA.
DR   PIR; A26879; A26879.
DR   PROSITE; PS00013; PROKAR_LIPOPROTEIN.
KW   HYDROLASE; GLYCOSIDASE; LIPOPROTEIN; SIGNAL.
FT   SIGNAL        1     19
FT   CHAIN        20   1096       PULLULANASE.
FT   LIPID        20     20       N-ACYL DIGLYCERIDE.
SQ   SEQUENCE   1096 AA;  119335 MW;  5852107 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB
```

```
Initial Score     =       5  Optimized Score  =       5  Significance =  3.30
Residue Identity =    100%  Matches          =       5  Mismatches   =     0
Gaps              =       0  Conservative Substitutions               =     0

    SFSDFTDRTVSVIAGNSAVYDSRADAFRAAFGVALADAHWVDKTTLLWPGGENKPIVRLYYSHSSKVAADSN
  160       170       180       190       200       210       220       230

                                X   X
                                YPAFK
                                |||||
    GEFSDKYVKLTPTTVNQQVSMRFPHLASYPAFKLPDDVNVDELLQGDDGGIAESDGILSLSHPGADRRRAGR
        240       250       260   X   270       280       290       300

    YLCRRAEALSYGAQLTDSGVTFRVWAPTAQQVELVIYSADKKVIASHPMTRDSASGAWSWQ
       310       320       330       340       350       360
```

4. CELSA-3 (1-5)
   S12888 *DNA-binding protein II - Thermus aquaticus

```
ENTRY            S12888     #Type Protein
TITLE            *DNA-binding protein II - Thermus aquaticus
DATE             11-Apr-1992 #Sequence 11-Apr-1992 #Text 11-Apr-1992
PLACEMENT           0.0    0.0    0.0    0.0    0.0
COMMENT          *This entry is not verified.
SOURCE           Thermus aquaticus
REFERENCE
   #Authors      Zierer R., Choli D.
   #Journal      FEBS Lett. (1990) 273:59-62
   #Title        The primary structure of DNA binding protein II from
                   the extreme thermophilic bacterium Thermus
                   thermophilus.
   #Reference-number S12888
   #Accession    S12888
```

SUMMARY

SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 3.30
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
    AAKKTVTKADLVD@VA@ATGLKLLDVKAMVDALLAKVEEALANGSKV@LTGFGTFEVRKRKARTGVKPGTKE
            10        20        30        40        50        60        70

            X   X
            YPAFK
            |||||
    KIKIPAT@YPAFKPGKALKDKVK
          80    X   90
```

5. CELSA-3 (1-5)
DBH_THETH DNA-BINDING PROTEIN II.

```
ID   DBH_THETH      STANDARD;      PRT;    95 AA.
AC   P19436;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE   DNA-BINDING PROTEIN II.
OS   THERMUS AQUATICUS (SUBSP. THERMOPHILUS).
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   UNCERTAIN.
RN   [1]
RP   SEQUENCE.
RM   91032203
RA   ZIERER R., CHOLI D.;
RL   FEBS LETT. 273:59-62(1990).
CC   -!- FUNCTION: THIS PROTEIN BELONGS OT THE HISTONE LIKE FAMILY OF
CC       PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
CC       DNA AND TO STABILIZE DNA FROM DENATURATION UNDER EXTREME
CC       ENVIRONMENTAL CONDITIONS.
CC   -!- SUBUNIT: HOMODIMER.
DR   PIR; S12888; S12888.
DR   PROSITE; PS00045; HISTONE_LIKE.
KW   DNA-BINDING; DNA CONDENSATION.
SQ   SEQUENCE   95 AA;  10163 MW;  48066 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB
```

Initial Score = 5 Optimized Score = 5 Significance = 3.30
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
    AAKKTVTKADLVD@VA@ATGLKLLDVKAMVDALLAKVEEALANGSKV@LTGFGTFEVRKRKARTGVKPGTKE
            10        20        30        40        50        60        70

            X   X
            YPAFK
            |||||
    KIKIPAT@YPAFKPGKALKDKVK
          80    X   90
```

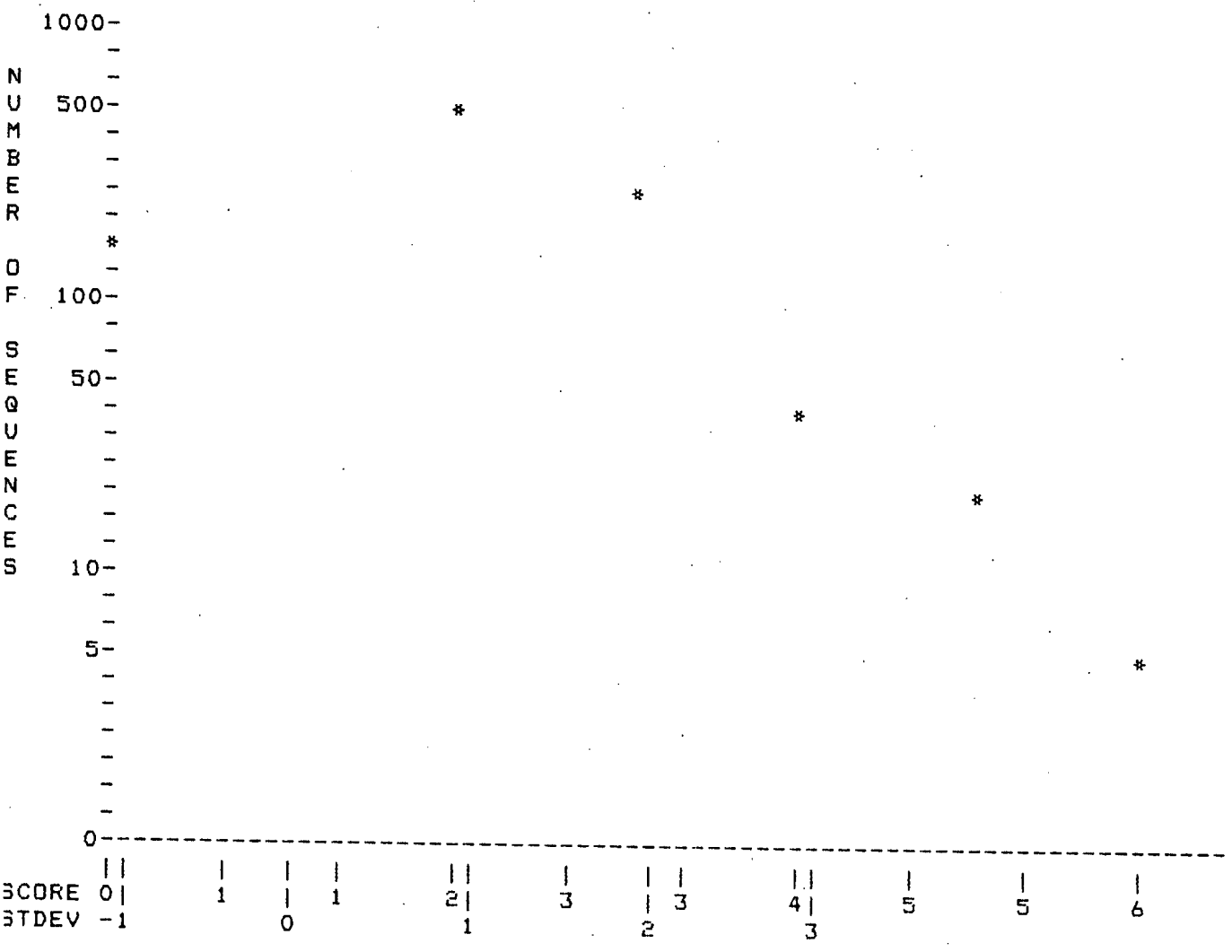
O| |O IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-align.res made by alexk on Thu 25 Feb 93 10:44:21-PST.

Query sequence being compared: CELSA-1 (1-6)
Number of sequences searched: 890 (interrupted)
Number of scores above cutoff: 757

Results of the initial comparison of CELSA-1 (1-6) with:
File : *.pep



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation

Times:	CPU	Total Elapsed
	00:00:05.04	00:00:07.00

Number of residues:	442959
Number of sequences searched:	890
Number of scores above cutoff:	757

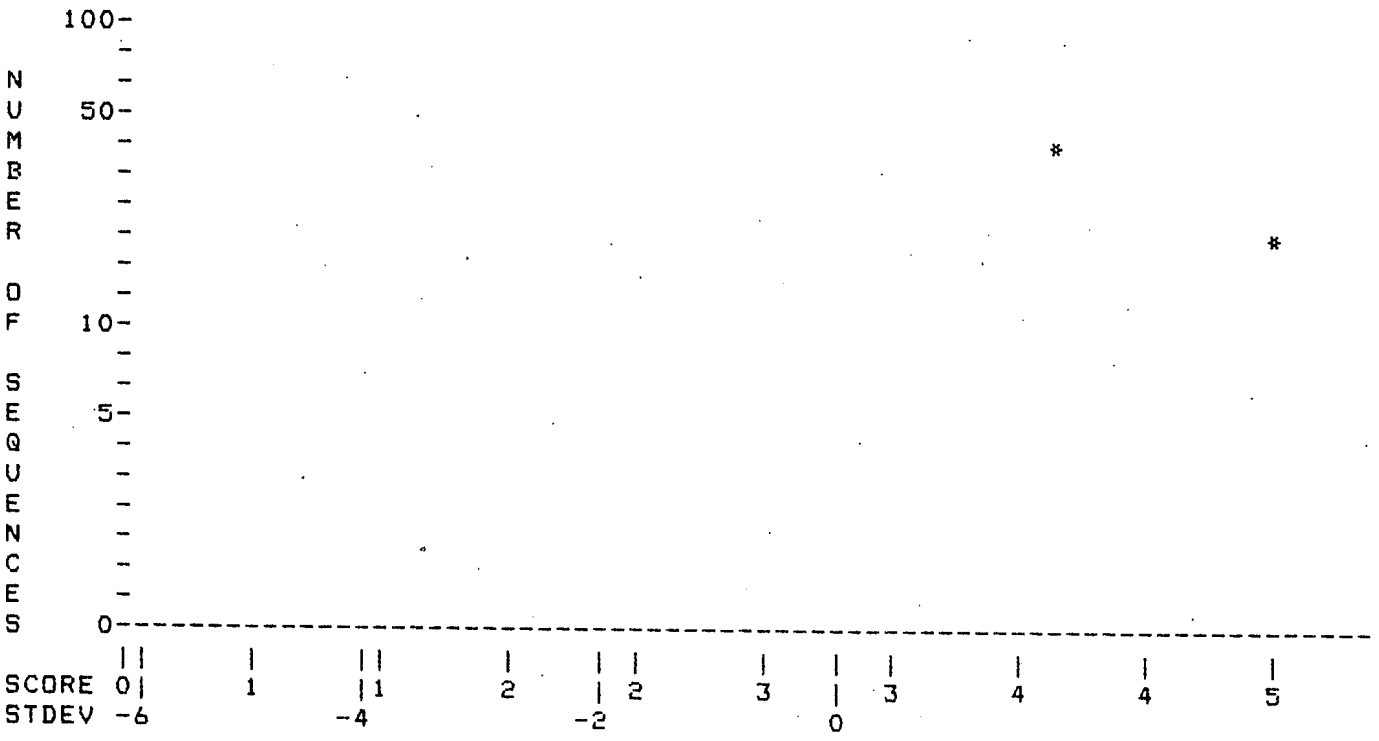
```
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-4-align.res made by alexk on Thu 25 Feb 93 10:51:58-PST.


Query sequence being compared:        CELSA-4 (1-5)
Number of sequences searched:                    50
Number of scores above cutoff:                   50

      Results of the initial comparison of CELSA-4 (1-5) with:
        File : celsa-4.pep
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	4	5	0.48

Times:	CPU	Total Elapsed
	00:00:00.01	00:00:00.00

Number of residues:	8503
Number of sequences searched:	50
Number of scores above cutoff:	50

Significance is calculated based on initial score.

17 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. S20590	*Sialidase - Actinomyces visc	913	5	5	2.09	0
2. A33827	*Regulatory protein ral2 - Ye	611	5	5	2.09	0
3. RAL2_SCHPO	RAL2 PROTEIN.	611	5	5	2.09	0
4. WMCVFM	Inclusion body matrix protein	512	5	5	2.09	0
5. IBMP_FMVD	INCLUSION BODY MATRIX PROTEIN	512	5	5	2.09	0
6. A30828	Steroid 17alpha-monooxygenase	507	5	5	2.09	0
7. S16719	*Steroid 17alpha-monooxygenas	507	5	5	2.09	0
8. CPT1_RAT	CYTOCHROME P450 XVIIA1 (P450-	507	5	5	2.09	0
9. JH0594	Vasoactive intestinal polypep	459	5	5	2.09	0
10. S16562	*nolF protein - Rhizobium mel	367	5	5	2.09	0
11. NOLF_RHIME	NODULATION PROTEIN NOLF.	367	5	5	2.09	0
12. A27659	Cytochrome P450 17 - Rat (fra	237	5	5	2.09	0
13. A33980	Steroid 17alpha-monooxygenase	235	5	5	2.09	0
14. S18659	*Hypothetical protein - Mycop	148	5	5	2.09	0
15. R20793	CDR-grafted, humanised heavy	146	5	5	2.09	0
16. S06727	*Hypothetical protein 1 (mini	122	5	5	2.09	0
17. YM2_STRCO	MINI-CIRCLE HYPOTHETICAL 13.3	122	5	5	2.09	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
18. A35776	*RecQ protein - Escherichia c	5	4	4	0.00	0
19. S04171	aadA protein - Klebsiella pne	23	4	4	0.00	0
20. RP30_YEAST	RIBOSOMAL PROTEIN RP30 (FRAGM	25	4	4	0.00	0

1. CELSA-4 (1-5)
   S20590 *Sialidase - Actinomyces viscosus #EC-number

ENTRY S20590 #Type Protein
TITLE *Sialidase - Actinomyces viscosus #EC-number 3.2.1.18
DATE 22-Jul-1992 #Sequence 22-Jul-1992 #Text 22-Jul-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
COMMENT *This entry is not verified.
SOURCE Actinomyces viscosus
REFERENCE
#Authors Henningsen M., Roggentin P., Schauer R.
#Journal Biol. Chem. Hoppe-Seyler (1991) 372:1065-1072
#Title Cloning, sequencing and expression of the sialidase gene from Actinomyces viscosus DSM 43798.
#Reference-number S20590
#Accession S20590
#Cross-reference EMBL:X62276
SUMMARY #Molecular-weight 96216 #Length 913 #Checksum 4303
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 2.09
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

PMGTCSSPTTSARRTTATAAATTPNPNHIVQRRSTDGGKTWSAPTYIHQGTETGKKVGYSDPSYVVDHQTGT
320 330 340 350 360 370 380 390

```
                                    QAEVS
                                    |||||
    IFNFHVKSYDQGWGGSRGGTDPENRGIIQAEVSTSTDNGWTWTHRTITADITKDKPWTARFAASGQGIQIQH
          400       410       420  X    430       440       450       460

    GPHAGRLVQQYTIRTAGGPVQAVSVYSDDHGKTWQAGTPIGTGMDENKVVELSDGSLMLNS
         470       480       490       500       510       520
```

2. CELSA-4 (1-5)
   A33827 *Regulatory protein ral2 - Yeast

ENTRY	A33827 #Type Protein
TITLE	*Regulatory protein ral2 - Yeast (Schizosaccharomyces pombe)
DATE	19-Sep-1992 #Sequence 19-Sep-1992 #Text 19-Sep-1992
PLACEMENT	0.0 0.0 0.0 0.0 0.0
COMMENT	*This entry is not verified.
SOURCE	Schizosaccharomyces pombe
REFERENCE	
#Authors	Fukui Y., Miyake S., Satoh M., Yamamoto M.
#Journal	Mol. Cell. Biol. (1989) 9:5617-5622
#Title	Characterization of the Schizosaccharomyces pombe ral2 gene implicated in activation of the ras1 gene product.
#Reference-number	A33827
#Accession	A33827
#Cross-reference	GB:M30827
SUMMARY	#Molecular-weight 69847 #Length 611 #Checksum 9734
SEQUENCE	
COMMENT	Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score	= 5	Optimized Score	= 5	Significance	= 2.09
Residue Identity	= 100%	Matches	= 5	Mismatches	= 0
Gaps	= 0	Conservative Substitutions			= 0

```
    VVFGNKTRKLTQDYNLRQSNYDHIVFIELEGYGVYRKPQMGRVTERSEQLGKLLLNGISDMEILTIERMHIP
     380       390       400       410       420       430       440

                                    X   X
                                    QAEVS
                                    |||||
    CLSRMLYKRWPAFQKIMDRAVEKNQEAFQAEVSQLGPQLTDLPFSSIHSTGSRALYMPYSFETCSAFLHYIY
   450       460       470       480       490       500       510       520

    CGTLNGSYCTAKNLCNLLILCKGFEGLETFFAYIVHLLHGVLNRNNVKLIYETAALTGAKG
          530       540       550       560       570       580
```

3. CELSA-4 (1-5)
   RAL2_SCHPO RAL2 PROTEIN.

```
ID   RAL2_SCHPO     STANDARD;      PRT;   611 AA.
AC   P15258;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE   RAL2 PROTEIN.
GN   RAL2.
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90066514
RA   FUKUI Y., MIYAKE S., SATOH M., YAMAMOTO M.;
```

CC -!- FUNCTION: IMPLICATED IN ACTIVATION OF RAS1 PROTEIN.
DR EMBL; M30827; SPRAL2.
DR PIR; A33827; A33827.
SQ SEQUENCE 611 AA; 69847 MW; 1910377 CN;
CC -!- Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 2.09
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

VVFGNKTRKLTQDYNLRQSNYDHIVFIELEGYGVYRKPQMGRVTERSEQLGKLLLNGISDMEILTIERMHIP
380 390 400 410 420 430 440

X X
QAEVS
|||||
CLSRMLYKRWPAFQKIMDRAVEKNQEAFQAEVSQLGPQLTDLPFSSIHSTGSRALYMPYSFETCSAFLHYIY
450 460 470 480 490 500 510 520

CGTLNGSYCTAKNLCNLLILCKGFEGLETFFAYIVHLLHGVLNRNNVKLIYETAALTGAKG
530 540 550 560 570 580

4. CELSA-4 (1-5)
WMCVFM Inclusion body matrix protein - Figwort mosaic vir

ENTRY WMCVFM #Type Protein
TITLE Inclusion body matrix protein - Figwort mosaic virus
DATE 30-Sep-1991 #Sequence 30-Sep-1991 #Text 30-Jun-1992
PLACEMENT 2377.0 1.0 1.0 1.0 1.0
SOURCE figwort mosaic virus
ACCESSION S01284
REFERENCE
#Authors Richins R.D., Scholthof H.B., Shepherd R.J.
#Journal Nucleic Acids Res. (1987) 15:8451-8466
#Title Sequence of figwort mosaic virus DNA (caulimovirus group).
#Reference-number S01279
#Accession S01284
#Molecule-type DNA
#Residues 1-512 <RIC>
#Cross-reference EMBL:X06166
#Comment The translation of the nucleotide sequence is not given in this paper.
COMMENT This virus is a member of the group Caulimovirus.
SUPERFAMILY #Name caulimovirus inclusion body matrix protein
KEYWORDS matrix protein
SUMMARY #Molecular-weight 58207 #Length 512 #Checksum 1605
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 2.09
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

NLTPKSDKDKVKSSPVANGSGKDSTNPLNPVALGKSKMTILGQKQADEEEFKPDYLRAASNGQSWFAVYKGP
100 110 120 130 140 150 160

X X
QAEVS
|||||
NKEFFTEWEIVADICKKRQKSKRFRSKEQAEVSISLYNKDIQDPVNFLRPVKLVKEERAAQPLKFKAIAAEQ
170 180 190 X X 200 210 220 230

TIQFDEFRQIWEKSRLSDLEDGVQEKFYTNDSASKSTYTFVENAEPYLVHTAFRAGLAKVI

5. CELSA-4 (1-5)
IBMP_FMVD INCLUSION BODY MATRIX PROTEIN (VIROPLASMIN).

```
ID   IBMP_FMVD      STANDARD;      PRT;   512 AA.
AC   P09524;
DT   01-MAR-1989 (REL. 10, CREATED)
DT   01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   INCLUSION BODY MATRIX PROTEIN (VIROPLASMIN).
GN   VI.
OS   FIGWORT MOSAIC VIRUS (STRAIN DXS) (FMV).
OC   VIRIDAE; DS-DNA NONENVELOPED VIRUSES; CAULIMOVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   88040466
RA   RICHINS R.D., SCHOLTHOF H.B., SHEPHERD R.J.;
RL   NUCLEIC ACIDS RES. 15:8451-8466(1987).
CC   -!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC       POLYCISTRONIC MRNA'S DERIVED FROM FIGWORT MOSAIC VIRUS.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC INCLUSION BODIES.
CC   -!- THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION
CC       ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC   -!- SIMILARITY: HIGH, WITH OTHER CAULIMOVIRUS VIROPLASMIN.
DR   EMBL; X06166; CAFMVXX.
DR   PIR; S01284; WMCVFM.
KW   TRANS-ACTING FACTOR; TRANSLATION REGULATION.
SQ   SEQUENCE   512 AA;  58207 MW;  1378914 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =  2.09
Residue Identity  =    100%  Matches          =       5  Mismatches   =     0
Gaps              =       0  Conservative Substitutions               =     0

    NLTPKSDKDKVKSSPVANGSGKDSTNPLNPVALGKSKMTILGQKQADEEEFKPDYLRAASNGQSWFAVYKGP
          100       110       120       130       140       150       160

                                  X   X
                                  QAEVS
                                  |||||
    NKEFFTEWEIVADICKKRQKSKRFRSKEQAEVSISLYNKDIQDPVNFLRPVKLVKEERAAQPLKFKAIAAEQ
        170       180       190 X   X 200       210       220       230

    TIQFDEFRQIWEKSRLSDLEDGVQEKFYTNDSASKSTYTFVENAEPYLVHTAFRAGLAKVI
      240       250       260       270       280       290
```

6. CELSA-4 (1-5)
A30828 Steroid 17alpha-monooxygenase cytochrome P450 17 -

```
ENTRY            A30828      #Type Protein
TITLE            Steroid 17alpha-monooxygenase cytochrome P450 17 -
                   Rat #EC-number 1.14.99.9
DATE             19-May-1989 #Sequence 19-May-1989 #Text 10-Aug-1992
PLACEMENT           0.0     0.0     0.0     0.0     0.0
SOURCE           Rattus norvegicus #Common-name Norway rat
ACCESSION        A30828\ A31359
REFERENCE
   #Authors      Dufau M.L.
   #Citation     submitted to GenBank, December 1988.
   #Reference-number A94511
   #Accession    A30828
   #Molecule-type mRNA
   #Residues     1-507 <DUF>
REFERENCE
```

#Authors Namiki M., Kitamura M., Buczko E., Durau M.L.
#Journal Biochem. Biophys. Res. Commun. (1988) 157:705-712
#Title Rat testis P-450-17-alpha cDNA: the deduced amino acid sequence, expression and secondary structural configuration.
#Reference-number A90154
#Accession A31359
#Molecule-type mRNA
#Residues 1-507 <NAM>
SUPERFAMILY #Name cytochrome P450
KEYWORDS endoplasmic reticulum\ heme\ membrane protein\ monooxygenase\ oxidoreductase
FEATURE
2-21 #Domain transmembrane <TM1>\
169-186 #Domain transmembrane <TM2>\
441 #Binding-site heme iron (Cys) (axial ligand) (predicted)
SUMMARY #Molecular-weight 57250 #Length 507 #Checksum 9025
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score	=	5	Optimized Score	=	5	Significance =	2.09
Residue Identity	=	100%	Matches	=	5	Mismatches =	0
Gaps	=	0	Conservative Substitutions			=	0

ENEWDQPDQFMPERFLDPTGSHLITPTQSYLPFGAGPRSCIGEALARQELFVFTALLLQRFDLDVSDDKQLP
410 420 430 440 450 460 470

X X
QAEVS
|||||
RLEGDPKVVFLIDPFKVKITVRQAWMDAQAEVST
480 490 500 X X

7. CELSA-4 (1-5)
S16719 *Steroid 17alpha-monooxygenase - Rat #EC-number

ENTRY S16719 #Type Protein
TITLE *Steroid 17alpha-monooxygenase - Rat #EC-number 1.14.99.9
DATE 15-Jun-1992 #Sequence 15-Jun-1992 #Text 15-Jun-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
COMMENT *This entry is not verified.
SOURCE Rattus norvegicus #Common-name Norway rat
REFERENCE
#Authors Fevold H.R., Lorence M.C., McCarthy J.L., Trant J.M., Kagimoto M., Waterman M.R., Mason J.I.
#Journal Mol. Endocrinol. (1989) 3:968-975
#Title Rat P450(17-alpha) from testis: characterization of a full-length cDNA encoding a unique steroid hydroxylase capable of catalyzing both Delta(4)- and Delta(5)-steroid-17,20-lyase reactions.
#Reference-number S16719
#Accession S16719
#Cross-reference EMBL:M31681
SUMMARY #Molecular-weight 57250 #Length 507 #Checksum 9025
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score	=	5	Optimized Score	=	5	Significance =	2.09
Residue Identity	=	100%	Matches	=	5	Mismatches =	0
Gaps	=	0	Conservative Substitutions			=	0

ENEWDQPDQFMPERFLDPTGSHLITPTQSYLPFGAGPRSCIGEALARQELFVFTALLLQRFDLDVSDDKQLP

```
                                    X   X
                                    QAEVS
                                    |||||
    RLEGDPKVVFLIDPFKVKITVRQAWMDAQAEVST
        480       490       500 X   X
```

8. CELSA-4 (1-5)
   CPT1_RAT CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (

```
ID   CPT1_RAT       STANDARD;      PRT;   507 AA.
AC   P11715;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE   CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA-
DE   HYDROXYLASE/17,20 LYASE).
GN   CYP17.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89295447
RA   FEVOLD H.R., LORENCE M.C., MCCARTHY J.L., TRANT J.M., KAGIMOTO M.,
RA   WATERMAN M.R., MASON J.I.;
RL   MOL. ENDOCRINOL. 3:968-975(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RM   89076306
RA   NAMIKI M., KITAMURA M., BUCZKO E., DUFAU M.L.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 157:705-712(1988).
RN   [3]
RP   SEQUENCE OF 271-507 FROM N.A.
RM   88280759
RA   NISHIHARA M., WINTERS C.A., BUZKO E., WATERMAN M.R., DUFAU M.L.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 154:151-158(1988).
RN   [4]
RP   SEQUENCE OF 273-507 FROM N.A.
RM   90046678
RA   MELLON S.H., VAISSE C.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 86:7775-7779(1989).
CC   -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC       MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC       COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC   -!- CATALYTIC ACTIVITY: A STEROID + AH(2) + O(2) = A 17-ALPHA-
CC       HYDROXYSTEROID + A + H(2)O.
DR   EMBL; M31681; RNP45017.
DR   EMBL; M22204; RNP450X.
DR   EMBL; M21208; RRCYPC17.
DR   EMBL; M27282; RNP450C1.
DR   PIR; A27659; A27659.
DR   PIR; A30828; A30828.
DR   PIR; S16719; S16719.
DR   PROSITE; PS00086; CYTOCHROME_P450.
KW   ELECTRON TRANSPORT; OXIDOREDUCTASE; MONOOXYGENASE; MEMBRANE;
KW   HEME; STEROIDOGENESIS.
FT   BINDING     441    441       HEME.
SQ   SEQUENCE   507 AA;  57250 MW;  1347075 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB
```

```
Initial Score    =      5  Optimized Score  =      5  Significance =  2.09
Residue Identity =   100%  Matches          =      5  Mismatches   =     0
```

```
ENEWDQPDQFMPERFLDPTGSHLITPTQSYLPFGAGPRSCIGEALARQELFVFTALLLQRFDLDVSDDKQLP
      410         420         430         440         450         460         470

                                   X   X
                                   QAEVS
                                   |||||
RLEGDPKVVFLIDPFKVKITVRQAWMDAQAEVST
     480         490         500 X   X
```

9. CELSA-4 (1-5)
JH0594 Vasoactive intestinal polypeptide receptor precurs

ENTRY JH0594 #Type Protein
TITLE Vasoactive intestinal polypeptide receptor precursor - Rat
DATE 17-Jul-1992 #Sequence 17-Jul-1992 #Text 17-Jul-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
SOURCE Rattus norvegicus #Common-name Norway rat
ACCESSION JH0594
REFERENCE (Lung)
#Authors Ishihara T., Shigemoto R., Mori K., Takahashi K., Nagata S.
#Journal Neuron (1992) 8:811-819
#Title Functional expression and tissue distribution of a novel receptor for vasoactive intestinal polypeptide.
#Reference-number JH0594
#Accession JH0594
#Molecule-type mRNA
#Residues 1-459 <ISH>
#Cross-reference GB:M86835
FEATURE
1-30 #Domain signal sequence (predicted) <SIG>\
31-459 #Protein vasoactive intestinal polypeptide receptor (predicted) <MAT>\
58,69,100,292 #Binding-site carbohydrate (Asn) (covalent) (predicted)\
146-168 #Domain transmembrane <TM1>\
176-195 #Domain transmembrane <TM2>\
218-241 #Domain transmembrane <TM3>\
256-277 #Domain transmembrane <TM4>\
295-318 #Domain transmembrane <TM5>\
344-363 #Domain transmembrane <TM6>\
376-395 #Domain transmembrane <TM7>
SUMMARY #Molecular-weight 52057 #Length 459 #Checksum 2598
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

```
Initial Score     =     5  Optimized Score    =     5  Significance =  2.09
Residue Identity  =  100%  Matches            =     5  Mismatches   =     0
Gaps              =     0  Conservative Substitutions               =     0

GIHYVNFAFFPDNFKAQVKMVFELVVGSFQGFVVAILYCFLNGEVQAELRRKWRRWHLQGVLGWSSKSQHPW
      360         370         380         390         400         410         420

                                   X   X
                                   QAEVS
                                   |||||
SGGHSATVSTQ SMLTRVSPGARPSSFQAEVSLV
      430         440         450 X   X
```

-- nodF protein - Rhizobium meliloti

ENTRY S16562 #Type Protein
TITLE *nolF protein - Rhizobium meliloti
DATE 11-Jan-1992 #Sequence 11-Jan-1992 #Text 11-Jan-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
COMMENT *This entry is not verified.
SOURCE Rhizobium meliloti
REFERENCE
#Authors Baev N., Endre G., Petrovics G., Banfalvi Z., Kondorosi A.
#Journal Mol. Gen. Genet. (1991) 228:113-124
#Title Six nodulation genes of nod box locus 4 in Rhizobium meliloti are involved in nodulation signal production: nodM codes for D-glucosamine synthetase.
#Reference-number S16561
#Accession S16562
#Cross-reference EMBL:X58632
SUMMARY #Molecular-weight 39541 #Length 367 #Checksum 9824
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 2.09
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
LTPIRRSTLTSRVSRRLLTSCSDRGRGQCRRSPRPFRKGSSRIGGDGAKSRGGCLSAQTELAEAVLERNTRL
     70        80        90       100       110       120       130

                              X   X
                              QAEVS
                              |||||
GERGAASEATRLAALADVLDLRAHVRSKQAEVSDAERSLSHAEVRAEFGGVIRARGVEEGQTVPLNTQLMTI
  140       150       160   X   170       180       190       200

VELNRLEVDAGVPTSRIPLIRLKQSVELMVEGFPGRTFSGEVARISPTADAGSRAVRVFIA
210       220       230       240       250       260
```

11. CELSA-4 (1-5)
NOLF_RHIME NODULATION PROTEIN NOLF.

ID NOLF_RHIME STANDARD; PRT; 367 AA.
AC P25196;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
DE NODULATION PROTEIN NOLF.
GN NOLF.
OS RHIZOBIUM MELILOTI.
OG PLASMID SYM PRME41B.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC RHIZOBIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AK 631;
RM 91360053
RA BAEV N., ENDRE G., PETROVICS G., BANFALVI Z., KONDOROSI A.;
RL MOL. GEN. GENET. 228:113-124(1991).
CC -!- FUNCTION: INVOLVED IN THE PRODUCTION OF NFB(CA)C-SPECIFIC
CC NODULATION SIGNAL MOLECULE.
DR EMBL; X58632; NOPRME41B.
DR PIR; S16562; S16562.
KW PLASMID; NODULATION.

Retrieved by alexk on Thu 25 Feb 93 10:42:00-PST using FastDB

```
Initial Score      =       5  Optimized Score  =        5  Significance =  2.09
Residue Identity =  100%  Matches              =        5  Mismatches     =     0
Gaps                 =       0  Conservative Substitutions                =     0

    LTPIRRSTLTSRVSRRLLTSCSDRGRGQCRRSPRPFRKGSSRIGGDGAKSRGGCLSAQTELAEAVLERNTRL
          70        80        90       100       110       120       130

                                            X    X
                                            QAEVS
                                            |||||
    GERGAASEATRLAALADVLDLRAHVRSKQAEVSDAERSLSHAEVRAEFGGVIRARSVEEGQTVPLNTQLMTI
      140       150       160   X    170       180       190       200

    VELNRLEVDAGVPTSRIPLIRLKQSVELMVEGFPGRTFSGEVARISPTADAGSRAVRVFIA
    210       220       230       240       250       260
```

12. CELSA-4 (1-5)
A27659 Cytochrome P450 17 - Rat (fragment)

```
ENTRY              A27659       #Type Protein (fragment)
TITLE              Cytochrome P450 17 - Rat (fragment)
ALTERNATE-NAME     cytochrome P450-17-alpha
DATE               31-Mar-1989 #Sequence 31-Mar-1989 #Text 10-Aug-1992
PLACEMENT            0.0     0.0     0.0     0.0     0.0
SOURCE             Rattus norvegicus #Common-name Norway rat
ACCESSION          A27659
REFERENCE
   #Authors        Nishihara M., Winters C.A., Buzko E., Waterman M.R.,
                     Dufau M.L.
   #Journal        Biochem. Biophys. Res. Commun. (1988) 154:151-158
   #Title          Hormonal regulation of rat Leydig cell cytochrome
                     P-450-17-alpha mRNA levels and characterization of
                     a partial length rat P-450-17-alpha cDNA.
   #Reference-number A27659
   #Accession      A27659
   #Molecule-type mRNA
   #Residues       1-237 &lt;NIS&gt;
   #Comment        The authors translated the codon GAT for residues
                     18, 131, and 208 as Glu, Asn, and Asn
                     respectively.
SUPERFAMILY        #Name cytochrome P450
KEYWORDS           heme\ monooxygenase\ oxidoreductase
FEATURE
   171                        #Binding-site heme iron (Cys) (axial
                                ligand)
SUMMARY                                   #Length 237  #Checksum  8451
SEQUENCE
COMMENT            Retrieved by alexk on Thu 25 Feb 93 10:42:01-PST using FastDB
```

```
Initial Score      =       5  Optimized Score  =        5  Significance =  2.09
Residue Identity =  100%  Matches              =        5  Mismatches     =     0
Gaps                 =       0  Conservative Substitutions                =     0

   ENEWDQPDQFMPERFLDPTCSHLITPTQSYLPFGAGPRSCIGEALARQELF[illegible]TALLLQRFDLDVSDDKQLP
        140       150       160       170       180       190       200

                                            X    X
                                            QAEVS
                                            |||||
   RLL[illegible]DPPVVFLIDPPKVSIT[illegible]RQANNDAQAEVSS
     [illegible]      [illegible]       230
```

A33980 Steroid 17alpha-monooxygenase cytochrome P450 17 -

ENTRY A33980 #Type Protein (fragment)
TITLE Steroid 17alpha-monooxygenase cytochrome P450 17 - Rat (fragment) #EC-number 1.14.99.9
DATE 31-Mar-1992 #Sequence 31-Mar-1992 #Text 10-Aug-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
SOURCE Rattus norvegicus #Common-name Norway rat
ACCESSION A33980
REFERENCE
#Authors Mellon S.H., Vaisse C.
#Journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:7775-7779
#Title cAMP regulates P450scc gene expression by a cycloheximide-insensitive mechanism in cultured mouse Leydig MA-10 cells.
#Reference-number A33980
#Accession A33980
#Molecule-type mRNA
#Residues 1-235 <MEL>
SUPERFAMILY #Name cytochrome P450
KEYWORDS heme\ monooxygenase\ oxidoreductase
FEATURE
169 #Binding-site heme iron (Cys) (axial ligand) (predicted)
SUMMARY #Length 235 #Checksum 7248
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:01-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 2.09
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
   ENEWD@PD@FMPERFLDPTGSHLITPT@SYLPFGAGPRSCIGEALAR@ELFVFTALLL@RFDLDVSDDK@LP
130        140        150        160        170        180        190        200

                                X    X
                                @AEVS
                                |||||
   RLEGDPKVVFLIDPFKVKITVR@AWMDA@AEVST
       210        220        230    X
```

14. CELSA-4 (1-5)
S18659 *Hypothetical protein - Mycoplasma hyorhinis (SGC3

ENTRY S18659 #Type Protein
TITLE *Hypothetical protein - Mycoplasma hyorhinis (SGC3)
DATE 02-Sep-1992 #Sequence 02-Sep-1992 #Text 02-Sep-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
COMMENT *This entry is not verified.
SOURCE Mycoplasma hyorhinis
REFERENCE
#Authors Yogev D., Rosengarten R., Watson-McKown R., Wise K.S.
#Journal EMBO J. (1991) 10:4069-4079
#Title Molecular basis of Mycoplasma surface antigenic variation: a novel set of divergent genes undergo spontaneous mutation of variable DNA repeats and 5' regulatory sequence.
#Reference-number S18631
#Accession S18659
#Molecule-type DNA

COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:01-PST using FastDB

Initial Score	=	5	Optimized Score	=	5	Significance	= 2.09
Residue Identity	=	100%	Matches	=	5	Mismatches	= 0
Gaps	=	0	Conservative Substitutions				= 0

```
                                          X   X
                                          @AEVS
                                          |||||
VDKLI@INHNN@DLVHL@VEINLE@@@VDI@D@EHL@AEVSLE@PVVLE@@@VNK@KLLLNL@N@DHKK@LL
        10        20        30       X 40        50        60        70

NL@N@DHKK@LLNL@N@DHKK@LLNL@N@DHKK@LLNL@N@DHKK@LLNL@N@DHKKLLKKKL@TKNPI
      80        90       100       110       120       130       140
```

15. CELSA-4 (1-5)
R20793 CDR-grafted, humanised heavy chain gH1.

```
ID   R20793 standard; Protein; 146 AA.
AC   R20793;
DT   19-MAY-1992  (first entry)
DE   CDR-grafted, humanised heavy chain gH1.
KW   murine monoclonal antibody; MAb; A5B7; humanised antibody; CEA;
KW   complementarity determining region.
OS   Homo sapiens.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT   /label= signal
FT   Protein         20..146
FT   /label= VH
FT   /note= "human LAY framework with A5B7 CDRs"
FT   Region          45..54
FT   /label= CDR1
FT   /note= "murine residues"
FT   Region          69..87
FT   /label= CDR2
FT   /note= "murine residues"
FT   Region          120..129
FT   /label= CDR3
FT   /note= "murine residues"
FT   Misc_difference 20
FT   /note= "murine residue"
FT   Misc_difference 67..68
FT   /note= "murine residues"
FT   Misc_difference 94..95
FT   /note= "murine residues"
FT   Misc_difference 98
FT   /note= "murine residue"
FT   Misc_difference 118
FT   /note= "murine residue"
PN   WO9201059-A.
PD   23-JAN-1992.
PF   05-JUL-1991; GO1108.
PR   05-JUL-1990; GB-014932.
PR   21-DEC-1990; WO-G02017.
PR   05-JUL-1991; WO-G01108.
PA   (CELL-) CELLTECH LTD.
PI   Adair JR, Bodmer MW, Mountain A, Owens RJ;
DR   WPI; 92-056874/07.
DR   N-PSDB; G20987.
PT   New CDR-grafted and humanised antigen binding protein -
PT   - therapeutic and diagnostic use.
```

CC ... heavy chain sequence comprises a human framework (i.e. the LAY
CC region) which contains murine sequences (from the murine anti-CEA
CC A5B7 MAb) in the CDRs and at other positions predicted to be
CC important for antigen-binding and at which human and A5B7 sequences
CC differ. (See 020984 for A5B7 heavy chain coding sequence).
SQ Sequence 146 AA;
SQ 7 A; 7 R; 4 N; 4 D; 0 B; 2 C; 6 Q; 6 E; 0 Z; 18 G; 1 H;
SQ 3 I; 14 L; 6 K; 3 M; 9 F; 3 P; 16 S; 13 T; 5 W; 9 Y; 10 V;
CC Retrieved by alexk on Thu 25 Feb 93 10:42:01-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 2.09
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

LFFLSVTTGVHSEVQLLESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKGLEWLGFIGNKANGYTT
10 20 30 40 50 60 70

X X
QAEVS
|||||
EYSASVKGRFTISRDKSKSTLYLQMNGLQAEVSAIYYCTRDRGLRFYFDYWGQGTLVTVSSASTKGP
80 90 100 110 X 120 130 140

16. CELSA-4 (1-5)
S06727 *Hypothetical protein 1 (minicircle) - Streptomyce

ENTRY S06727 *Type Protein
TITLE *Hypothetical protein 1 (minicircle) - Streptomyces coelicolor
DATE 15-Jun-1992 *Sequence 15-Jun-1992 *Text 15-Jun-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
COMMENT *This entry is not verified.
SOURCE Streptomyces coelicolor
REFERENCE
*Authors Henderson D.J., Lydiate D.J., Hopwood D.A.
*Journal Mol. Microbiol. (1989) 3:1307-1318
*Title Structural and functional analysis of the mini-circle, a transposable element of Streptomyces coelicolor A3(2).
*Reference-number S06727
*Accession S06727
*Cross-reference EMBL:X15942
SUMMARY *Molecular-weight 13374 *Length 122 *Checksum 9249
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:42:01-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 2.09
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X X
QAEVS
|||||
MTLLGLVQHMAEVERNWFQRVFAGQNVPPVFGESNHDGFALKSGRGLDEAVAAWQAEVSRGRELIADAGLDD
10 20 30 40 50 X 60 70

SGHLSEQEAGHVGDQGVSLRWIMVHMIEEYARHNGHADLIREQIDGTTGA
80 90 100 110 120

17. CELSA-4 (1-5)
YM2_STRCO MINI-CIRCLE HYPOTHETICAL [illegible]

```
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE   MINI-CIRCLE HYPOTHETICAL 13.3 KD PROTEIN.
OS   STREPTOMYCES COELICOLOR.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RM   90136057
RA   HENDERSON D.J., LYDIATE D.J., HOPWOOD D.A.;
RL   MOL. MICROBIOL. 3:1307-1318(1989).
DR   EMBL; X15942; SCMINCIR.
DR   PIR; S06727; S06727.
KW   TRANSPOSABLE ELEMENT; HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   122 AA;  13374 MW;  65218 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:42:01-PST using FastDB
```

Initial Score	=	5	Optimized Score	=	5	Significance	= 2.09
Residue Identity	=	100%	Matches	=	5	Mismatches	= 0
Gaps	=	0	Conservative Substitutions				= 0

```
                                                                X    X
                                                                @AEVS
                                                                |||||
    MTLLGLV@HMAEVERNWF@RVFAG@NVPPVFGESNHDGFALKSGRGLDEAVAAW@AEVSRGRELIADAGLDD
            10        20        30        40        50    X   60        70

    SGHLSE@EAGHVGD@GVSLRWIMVHMIEEYARHNGHADLIRE@IDGTTGA
          80        90       100       110       120
```

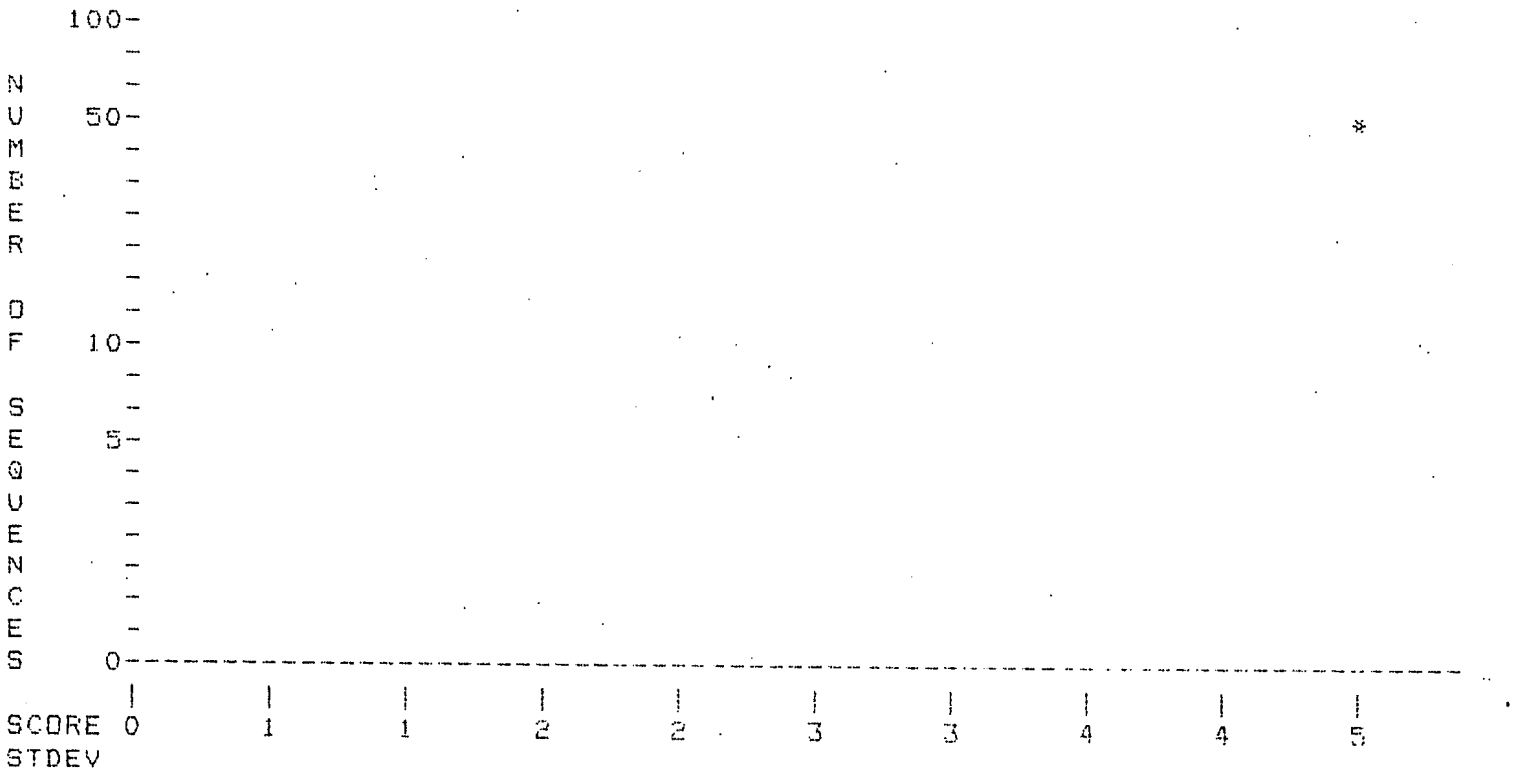
IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-14-align.res made by alexk on Thu 25 Feb 93 11:15:30-PST.

Query sequence being compared: CELSA-14 (1-5)
Number of sequences searched: 50
Number of scores above cutoff: 50

Results of the initial comparison of CELSA-14 (1-5) with:
File : celsa-14.pep



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	5	6	0.00

Times:	CPU	Total Elapsed
	00:00:01.03	00:00:01.00

Number of residues:	45939
Number of sequences searched:	50
Number of scores above cutoff:	50

... is calculated based on initial score.

50 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	S18268	*alpha-Aminoadipyl-L-cysteiny	3649	5	5	0.00	0
2.	ACVS_NOCLA	L-(ALPHA-AMINOADIPYL)-L-CYSTE	3649	5	5	0.00	0
3.	S12332	Ubiquitin--protein ligase - Y	1950	5	5	0.00	0
4.	UBR1_YEAST	N-END-RECOGNIZING PROTEIN (UB	1950	5	5	0.00	0
5.	RRWGNV	RNA-directed RNA polymerase -	1643	5	5	0.00	0
6.	VOR1_NMV	186 KD PROTEIN (ORF 1).	1643	5	5	0.00	0
7.	WMWGPV	RNA-directed RNA polymerase -	1643	5	5	0.00	0
8.	S14005	*Hypothetical protein, 166K -	1456	5	5	0.00	0
9.	VOR1_PVX	165 KD PROTEIN (ORF 1).	1456	5	5	0.00	0
10.	VOR1_PVXCP	165 KD PROTEIN (ORF 1).	1456	5	5	0.00	0
11.	VOR1_PVXX3	165 KD PROTEIN (ORF 1).	1456	5	5	0.00	0
12.	VGIHJ2	E2 glycoprotein precursor - M	1456	5	5	0.00	0
13.	VGL2_CVM4	E2 GLYCOPROTEIN PRECURSOR (SP	1376	5	5	0.00	0
14.	VGIH59	E2 glycoprotein precursor - M	1376	5	5	0.00	0
15.	VGL2_CVMA5	E2 GLYCOPROTEIN PRECURSOR (SP	1324	5	5	0.00	0
16.	VGIHMJ	E2 glycoprotein precursor - M	1324	5	5	0.00	0
17.	VGL2_CVMJH	E2 GLYCOPROTEIN PRECURSOR (SP	1235	5	5	0.00	0
18.	A40986	*M-cadherin - Mouse (fragment	1235	5	5	0.00	0
19.	SAHU4F	Cell surface antigen 4F2 heav	730	5	5	0.00	0
20.	A39984	*Cell surface antigen 4F2 hea	529	5	5	0.00	0

(Last row Length column also shows 529.)

1. CELSA-14 (1-5)
S18268 *alpha-Aminoadipyl-L-cysteinyl-D-valine synthetase

```
ENTRY              S18268      #Type Protein
TITLE              *alpha-Aminoadipyl-L-cysteinyl-D-valine synthetase -
                     Streptomyces lactamdurans
DATE               02-Apr-1992 #Sequence 02-Apr-1992 #Text 02-Apr-1992
PLACEMENT             0.0     0.0     0.0     0.0     0.0
COMMENT            *This entry is not verified.
SOURCE             Streptomyces lactamdurans
REFERENCE
   #Authors        Martin J.F.
   #Citation       submitted to the EMBL Data Library, January 1991
   #Reference-number S18268
   #Accession      S18268
   #Cross-reference EMBL:X57310
SUMMARY        #Molecular-weight 404084  #Length 3649  #Checksum  2296
SEQUENCE
COMMENT            Retrieved by alexk on Thu 25 Feb 93 10:29:01-PST using FastDB

Initial Score     =     5  Optimized Score   =     5  Significance =  0.00
Residue Identity  =  100%  Matches           =     5  Mismatches   =     0
Gaps              =     0  Conservative Substitutions                =     0

    ALSSRDRAYVTYTSGTTGVPKGVPKYHYSVVNSITDLSERYDMRRPGTERVALFASYVFEPHLRQTLIALIN
    400       410       420       430       440       450       460

                                     X   X
                                     YLNAT
                                     |||||
    EQTLVIVPDDVRLDPDLFPEVIERHGVTYLNATGSVLAHFDLRRLASLARL
   470       480       490       500 Y     510
```

2. CELSA-14 (1-5) **Best Available Copy**
ACVS_NOCLA L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHET

```
ID   ACVS_NOCLA      STANDARD;      PRT:  3649 AA.
AC   P27743;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHETASE (EC 6.-.-.-)
DE   (ACV SYNTHETASE) (ACVS).
GN   PCBAB.
OS   NOCARDIA LACTAMDURANS.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIOFORM.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VAR LC 411;
RM   92065808
RA   COQUE J.J.R., MARTIN J.F., CALZADA J.G., LIRAS P.;
RL   MOL. MICROBIOL. 5:1125-1133(1991).
CC   -!- FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF ACV ARE ACTIVATED
CC       AS AMIONACYL-ADENYLATES WITH PEPTIDE BONDS FORMED THROUGH THE
CC       PARTICIPATION OF AMINO ACID THIOLESTER INTERMEDIATES.
CC   -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND
CC       CEPHALOSPORIN.
CC   -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC       COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR   EMBL; X57310; NLPCBABC.
DR   PIR; S18268; S18268.
KW   LIGASE; ANTIBIOTIC BIOSYNTHESIS; DUPLICATION.
SQ   SEQUENCE   3649 AA;  404079 MW;  2.019611E+07 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score     =      5  Optimized Score  =      5  Significance =  0.00
Residue Identity  =   100%  Matches          =      5  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    ALSSRDRAYVTYTSGTTGVPKGVPKYHYSVVNSITDLSERYDMRRPGTERVALFASYVFEPHLRQTLIALIN
    400       410       420       430       440       450       460

                                  X   X
                                  YLNAT
                                  |||||
    EQTLVIVPDDVRLDPDLFPEYIERHGVTYLNATGSVLQHFDLRRCASLKRLLLVGEELTASGLRQLREKFAG
470       480       490       500 X     510       520       530       540

    RVVNEYAFTEAAFVTAVKEFGPGVTERRDRSIGRPLRNVKWYVLSQGLKQLPIGAIGELYI
          550       560       570       580       590       600
```

3. CELSA-14 (1-5)
S12332 Ubiquitin--protein ligase - Yeast (Saccharomyces

```
ENTRY          S12332      #Type Protein
TITLE          Ubiquitin--protein ligase - Yeast (Saccharomyces
                 cerevisiae) #EC-number 6.3.2.19
DATE           16-Sep-1992 #Sequence 16-Sep-1992 #Text 29-Sep-1992
PLACEMENT        0.0     0.0     0.0     0.0     0.0
SOURCE         Saccharomyces cerevisiae
ACCESSION      S12332
REFERENCE
  #Authors     Bartel B., Wünning I., Varshavsky A.
  #Journal     EMBO J. (1990) 9:3179-3189
  #Title       [illegible]
  #Reference-Number [illegible]
```

```
      #Residues      1-1950 <BAR>
      #Cross-reference EMBL:X53747
   GENETIC
      #Map-position   15
      #Name           UBR1
   SUPERFAMILY     #Name ubiquitin--protein ligase
   KEYWORDS        protein degradation
   SUMMARY      #Molecular-weight 224836  #Length 1950  #Checksum  7669
   SEQUENCE
   COMMENT         Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

 Initial Score     =      5  Optimized Score  =      5  Significance =  0.00
 Residue Identity  =   100%  Matches          =      5  Mismatches   =     0
 Gaps              =      0  Conservative Substitutions               =     0

     ATTALR@GVPDNVHIDLLTSRIDGEGRAMLKCS@DLSSVLGGFFAV@TNGLSATLTSWSEYLH@ETCKYIIL
       330       340       350       360       370       380       390

                                    X   X
                                    YLNAT
                                    |||||
     WITHCLNIPNSSF@TTFRNMMGKTLCSEYLNATECRDMTPVVEKYFSNKFDKNDPYRYIDLSILADGN@IPL
     400       410       420       X 430       440       450       460

     GHHKILPESSTHSLSPLINDVETPTSRTYSNTRL@HILYFDNRYWKRLRKDI@NVIIPTLA
   470       480       490       500       510       520       530
```

4. CELSA-14 (1-5)
   UBR1_YEAST   N-END-RECOGNIZING PROTEIN (UBI@UITIN-PROTEIN LIGAS

```
 ID   UBR1_YEAST      STANDARD;      PRT;  1950 AA.
 AC   P19812;
 DT   01-FEB-1991 (REL. 17, CREATED)
 DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
 DE   N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N-
 DE   RECOGNIN).
 GN   UBR1.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=GRF88 (S288C);
 RM   91006011
 RA   BARTEL B., WUENNING I., VARSHAVSKY A.;
 RL   EMBO J. 9:3179-3189(1990).
 CC   -!- FUNCTION: UBR1 IS THE RECOGNITION COMPONENT OF THE N-END RULE
 CC       PATHWAY. UBR1 BINDS TO PROTEINS BEARING AMINO-TERMINAL RESIDUES
 CC       THAT ARE DESTABILIZING ACCORDING TO THE N-END RULE, BUT DOES NOT
 CC       BIND TO OTHERWISE IDENTICAL PROTEINS BEARING STABILIZING AMINO-
 CC       TERMINAL RESIDUES.
 DR   EMBL; X53747; SCUBR1G.
 DR   PIR; S12332; S12332.
 KW   UBIQUITIN CONJUGATION.
 SQ   SEQUENCE   1950 AA;  224836 MW;  1.833403E+07 CN;
 CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02 PST using FastDB

Initial Score     =      5  Optimized Score  =      5  Significance =  0.00
Residue Identity  =   100%  Matches          =      5  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    ATTALR@GVPDNVHIDLLTSRIDGEGRAMLKCS@DLSSVLGGFFAV@TNGLSATLTSWSEYLH@ETCKYIIL
      330       340       350       360       370       380       390
```

```
                                                    X
                                                   YLNAT
                                                   |||||
    WITHCLNIPNSSF@TTFRNMMGKTLCSEYLNATECRDMTPVVEKYFSNKFDKNDPYRYIDLSILADGN@IFL
    400       410       420       X 430       440       450       460

    GHHKILPESSTHSLSPLINDVETPTSRTYSNTRL@HILYFDNRYWKRLRKDI@NVIIPTLA
470       480       490       500       510       520       530
```

5. CELSA-14 (1-5)
   RRWGNV RNA-directed RNA polymerase - Narcissus mosaic vir

```
ENTRY                RRWGNV      #Type Protein
TITLE                RNA-directed RNA polymerase - Narcissus mosaic virus
                       #EC-number 2.7.7.48
ALTERNATE-NAME       RNA replicase
DATE                 30-Sep-1992 #Sequence 30-Sep-1992 #Text 30-Sep-1992
PLACEMENT             364.0     3.0     1.0     1.0     1.0
SOURCE               narcissus mosaic virus
ACCESSION            JT0470
REFERENCE
    #Authors         Zuideme D., Linthorst H.J.M., Huisman M.J., Asjes
                       C.J., Bol J.F.
    #Journal         J. Gen. Virol. (1989) 70:267-276
    #Title           Nucleotide sequence of narcissus mosaic virus RNA.
    #Reference-number JT0470
    #Accession       JT0470
    #Molecule-type genomic RNA
    #Residues        1-1643 <ZUI>
    #Cross-reference GB:D00405
COMMENT              This virus is a member of the Potexvirus group.
SUPERFAMILY          #Name eggplant mosaic virus RNA-directed RNA
                       polymerase
KEYWORDS             nucleotidyltransferase
SUMMARY          #Molecular-weight 186303  #Length 1643  #Checksum  8014
SEQUENCE
COMMENT              Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB.
```

Initial Score	=	5	Optimized Score	=	5	Significance	= 0.00
Residue Identity	=	100%	Matches	=	5	Mismatches	= 0
Gaps	=	0	Conservative Substitutions				= 0

```
    VTPTVLLRNDW@TKLPILPADVFKTFEKSVI@PCNPILVFDDYTKLPPGLIESVVMHH@NVVFIILTGDNR@
      900       910       920       930       940       950       960

                                      X    X
                                     YLNAT
                                     |||||
    SVYHETNPEAYIAALPEAVEIFSPYCEFYLNATHRNVKDLANKLGVYSERECALKVNFASHHLKASRIPMLV
     970       980       990       X 1000      1010      1020      1030

    PSTMKRNAMFDMGHHSMTYAGC@GLTAPKI@ILLDNHT@F@SERVLYTCLSRAVDRIHFIN
1040      1050      1060      1070      1080      1090
```

6. CELSA-14 (1-5)
   VOR1_NMV 186 KD PROTEIN (ORF 1).

```
ID   VOR1_NMV        STANDARD;      PRT;  1643 AA.
AC   P15095;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   [illegible]
DT   [illegible]
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89279206
RA   ZUIDEMA D., LINTHORST H.J.M., HUISMAN M.J., ASJES C.J., BOL J.F.;
RL   J. GEN. VIROL. 70:267-276(1989).
CC   -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC       POSSIBLY FUNCTIONS AS A NTP-BINDING HELICASE.
DR   EMBL; D00405; NMV.
DR   PIR; JT0470; JT0470.
KW   NUCLEOTIDE-BINDING; HELICASE; RNA REPLICATION.
SQ   SEQUENCE   1643 AA;  186304 MW;  1.392861E+07 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02 PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0

    VTPTVLLRNDWQTKLPILPADVFKTFEKSVIQPCNPILVFDDYTKLPPGLIESVVMHHQNVVFIILTGDNRQ
       900       910       920       930       940       950       960

                                    X   X
                                    YLNAT
                                    |||||
    SVYHETNPEAYIAALPEAVEIFSPYCEFYLNATHRNVKDLANKLGVYSEREGKLKVNFASHHLKASRIPMLV
     970       980       990     X 1000      1010      1020      1030

    PSTMKRNAMFDMGHHSMTYAGCQGLTAPKIQILLDNHTQFCSERVLYTCLSRAVDRIHFIN
  1040      1050      1060      1070      1080      1090


7.  CELSA-14 (1-5)
    WMWGPV        RNA-directed RNA polymerase - Potato virus X (stra

ENTRY             WMWGPV      #Type Protein
TITLE             RNA-directed RNA polymerase - Potato virus X (strain
                    X3) #EC-number 2.7.7.48
ALTERNATE-NAME    RNA replicase
DATE              30-Jun-1990 #Sequence 30-Jun-1990 #Text 30-Sep-1992
PLACEMENT          364.0     4.0     1.0     1.0     1.0
SOURCE            potato virus X, PVX
HOST              Nicotiana tabacum cv. Samsun #Common-name tobacco
ACCESSION         JA0102
REFERENCE
    #Authors      Huisman M.J., Linthorst H.J.M., Bol J.F.,
                    Cornelissen B.J.C.
    #Journal      J. Gen. Virol. (1988) 69:1789-1798
    #Title        The complete nucleotide sequence of potato virus X
                    and its homologies at the amino acid level with
                    various plus-stranded RNA viruses.
    #Reference-number JA0102
    #Accession    JA0102
    #Molecule-type mRNA
    #Residues     1-1456 <HUI>
    #Cross-reference GB:M31541
COMMENT           This virus is a member of the Potexvirus group.
SUPERFAMILY       #Name eggplant mosaic virus RNA-directed DNA
                    polymerase
KEYWORDS          nucleotidyltransferase
SUMMARY      #Molecular-weight 155605  #Length 1456  #Checksum  6078
SEQUENCE
COMMENT           Retrieved by alexk on Thu 25 Feb 93 10:29:02 PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0
```

```
VLPTNELRLDWSKKVPNTEPYMFKTYEKALIGGTGSIVIFDDYSKLPPGYIEALVCFYSKIKLIILTGDSR@
      770       780       790       800       810       820       830

                                X   X
                                YLNAT
                                |||||
SVYHETAEDASIRHLGPATEYFSKYCRYYLNATHRNKKDLANMLGVYSERTGVTEISMSAEFLEGIPTLVPS
     840       850       860     X 870       880       890       900

DEKRKLYMGTGRNDTFTYAGC@GLTKPKV@IVLDHNT@VCSANVMYTALSRATDRIHFVNT
   910       920       930       940       950       960
```

8. CELSA-14 (1-5)
   S14005 *Hypothetical protein, 166K - Potato virus X

```
ENTRY           S14005     #Type Protein
TITLE           *Hypothetical protein, 166K - Potato virus X
DATE            16-Apr-1992 #Sequence 16-Apr-1992 #Text 16-Apr-1992
PLACEMENT          0.0    0.0    0.0    0.0    0.0
COMMENT         *This entry is not verified.
SOURCE          potato virus X, PVX
REFERENCE
  #Authors      Orman B.E., Celnik R.M., Mandel A.M., Torres H.N.,
                  Mentaberry A.N.
  #Journal      Virus Res. (1990) 16:293-306
  #Title        Complete cDNA sequence of a South American isolate
                  of potato virus X.
  #Reference-number S14005
  #Accession    S14005
  #Cross-reference EMBL:X55802
SUMMARY      #Molecular-weight 165300  #Length 1456  #Checksum  9959
SEQUENCE
COMMENT         Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0

VLPTNELRLDWSKKVPNTEPYMFKTYEKALIGGTGSIVIFDDYSKLPPGYIEALVSFSTKIKLIILTGDSR@
      770       780       790       800       810       820       830

                                X   X
                                YLNAT
                                |||||
SVYHETSDDASIRHLGPATEVFAKYCRYYLNATHRNKKDLANMLGVYSERTGTTEISMSSEFLEGVPTLVPS
     840       850       860     X 870       880       890       900

DEKRRLYMGTGRNDTFTYAGC@GLTKPKV@IVLDHNT@VCSANVMYSALSRATDRIHFINT
   910       920       930       940       950       960
```

9. CELSA-14 (1-5)
   VOR1_PVX 165 KD PROTEIN (ORF 1).

```
ID   VOR1_PVX       STANDARD;      PRT;  1456 AA.
AC   P09395;
DT   01-MAR-1989 (REL. 10, CREATED)
DT   01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   165 KD PROTEIN (ORF 1).
OS   POTATO VIRUS X (P. X).
OC   VIRUSES; SS-RNA [illegible]
RN   [1]
```

RN 87083520
RA SKRYABIN K.G., KRAEV A.S., MOROZOV S.Y., ROZANOV M.N., CHERNOV B.K.,
RA LUKASHEVA L.I., ATABEKOV J.G.;
RL NUCLEIC ACIDS RES. 16:10929-10930(1988).
CC -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC POSSIBLY FUNCTIONS AS A NTP-BINDING HELICASE.
DR EMBL; X05198; POPVX3.
KW NUCLEOTIDE-BINDING; HELICASE; RNA REPLICATION.
FT NP_BIND 735 742 POTENTIAL.
SQ SEQUENCE 1456 AA; 165406 MW; 1.09471E+07 CN;
CC -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 0.00
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

VLPTNELRLDWSKKVPNTEPYMFKTYEKALIGGTGSIVIFDDYSKLPPGYIEALICFYSKIKLVILTGDSRQ
770 780 790 800 810 820 830

X X
YLNAT
|||||
SVYHETAEDASIRHLGPATEYFSKYCRYYLNATHRNKKDLANMLGVYSGERTGVTEISMSAEFLEGIPTLVPS
840 850 860 X 870 880 890 900

DEKRRLYMGTGRNDTFTYAGCQGLTKPKVQIVLDHNTQVCSANVMYTALSPATDRIHFVNT
910 920 930 940 950 960

10. CELSA-14 (1-5)
VOR1_PVXCP 165 KD PROTEIN (ORF 1).

ID VOR1_PVXCP STANDARD; PRT; 1456 AA.
AC P22591;
DT 01-AUG-1991 (REL. 19, CREATED)
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE 165 KD PROTEIN (ORF 1).
OS POTATO VIRUS X (STRAIN CP) (PVX).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; POTEXVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RM 90364772
RA ORMAN B.E., CELNIK R.M., MANDEL A.M., TORRES H.N., MENTABERRY A.N.;
RL VIRUS RES. 16:293-306(1990).
CC -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC POSSIBLY FUNCTIONS AS A NTP-BINDING HELICASE.
DR EMBL; X55802; POPOVX.
DR PIR; S14005; S14005.
KW NUCLEOTIDE-BINDING; HELICASE; RNA REPLICATION.
FT NP_BIND 735 742 POTENTIAL.
SQ SEQUENCE 1456 AA; 165301 MW; 1.0946B1E+07 CN;
CC -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 0.00
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

VLPTNELRLDWSKKVPNTEPYMFKTYEKALIGGTGSIVIFDDYSKLPPGYIEALICFYSKIKLVILTGDSRQ
770 780 790 800 810 820 830

X X
YLNAT
|||||

```
DEKRRLYMGTGRNDTFTYAGCGSLTKPKV@IVLDHNT@VCSANVMYTALSRATDRIHFINT
   910       920       930       940       950       960
```

11. CELSA-14 (1-5)
VOR1_PVXX3 165 KD PROTEIN (ORF 1).

```
ID   VOR1_PVXX3     STANDARD;      PRT;  1456 AA.
AC   P17779;
DT   01-AUG-1990 (REL. 15, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   165 KD PROTEIN (ORF 1).
OS   POTATO VIRUS X (STRAIN X3) (PVX).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; POTEXVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   88299944
RA   HUISMAN M.J., LINTHORST H.J.M., BOL J.F., CORNELISSEN B.J.C.;
RL   J. GEN. VIROL. 69:1789-1798(1988).
CC   -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC       POSSIBLY FUNCTIONS AS A NTP-BINDING HELICASE.
DR   EMBL; D00344; PVXX3.
DR   PIR; JA0102; WMWGPV.
KW   NUCLEOTIDE-BINDING; HELICASE; RNA REPLICATION.
FT   NP_BIND     735     742        POTENTIAL.
SQ   SEQUENCE   1456 AA;  165605 MW;  1.100152E+07 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB
```

```
Initial Score     =      5  Optimized Score  =      5  Significance =   0.00
Residue Identity  =   100%  Matches          =      5  Mismatches   =      0
Gaps              =      0  Conservative Substitutions               =      0

   VLPTNELRLDWSKKVPNTEPYMFKTYEKALIGGTGSIVIFDDYSKLPPGYIEALVCFYSKIKLIILTGDSRQ
         770       780       790       800       810       820       830

                                  X   X
                                  YLNAT
                                  |||||
   SVYHETAEDASIRHLGPATEYFSKYCRYYLNATHRNKKDLANMLGVYSERTGVTEISMSAEFLEGIPTLVPG
        840       850       860    X  870       880       890       900

   DEKRKLYMGTGRNDTFTYAGC@GLTKPKV@IVLDHNT@VCSANVMYTALSRATDRIHFVNT
      910       920       930       940       950       960
```

12. CELSA-14 (1-5)
VGIHJ2 E2 glycoprotein precursor - Murine hepatitis virus

```
ENTRY            VGIHJ2      #Type Protein
TITLE            E2 glycoprotein precursor - Murine hepatitis virus
                   (strain wild type MHV-4)
ALTERNATE-NAME   peplomer glycoprotein\ spike glycoprotein
INCLUDES         90B glycoprotein\ 90A glycoprotein
DATE             31-Mar-1991 #Sequence 31-Mar-1991 [illegible]
PLACEMENT        2231.0    4.0    1.0    3.0    1.0
SOURCE           murine hepatitis virus, MHV
ACCESSION        A33743
REFERENCE
   #Authors      Parker S.E., Gallagher T.M., Buchmeier [illegible]
   #Journal      Virology (1989) 173:[illegible]
   #Title        Sequence analysis reveals extensive [illegible]
```

```
     #Accession     A33748
     #Molecule-type genomic RNA
     #Residues      1-1376 <PAR>
  COMMENT           This virus is a member of the family Coronaviridae.
  SUPERFAMILY       #Name coronavirus E2 glycoprotein
  KEYWORDS          glycoprotein\ membrane protein
  FEATURE
     1-14                          #Domain signal sequence <SIG>\
     15-1376                       #Protein E2 glycoprotein <E2G>\
     15-769                        #Protein 90B glycoprotein <EGB>\
     770-1376                      #Protein 90A glycoprotein <EGA>\
     1321-1338                     #Domain transmembrane <TMN>\
     31,60,134,192,357,435,
     442,582,677,709,717,
     740,789,806,896,945,
     1178,1232,1242,1261,
     1277,1298,1370                #Binding-site carbohydrate (Asn)
                                     (covalent) (predicted)
  SUMMARY       #Molecular-weight 151881  #Length 1376  #Checksum  4481
  SEQUENCE
  COMMENT           Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0

                                                                  X    X
                                                                  YLNAT
                                                                  |||||
     MLFVFILLLPSCLGYIGDFRCIQTVNYNGNNASAPSISTEAVDVSKGLGTYYVLDRVYLNATLLLTGYYPVD
             10        20        30        40        50        60 X      70

     GSNYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKVQNLKTNTPTGATSYFPTIVIGSLFGNTSYTVVLEPY
           80        90        100       110       120       130       140

     NNIIMASVCTYTICQLPY
        150       160


13.  CELSA-14 (1-5)
     VGL2_CVM4     E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PE

  ID   VGL2_CVM4       STANDARD;       PRT;  1376 AA.
  AC   P22432;
  DT   01-AUG-1991 (REL. 19, CREATED)
  DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
  DT   01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
  DE   E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).
  GN   S.
  OS   MURINE CORONAVIRUS MHV (STRAIN WILD TYPE 4) (MHV-4).
  OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; CORONAVIRIDAE.
  RN   [1]
  RP   SEQUENCE FROM N.A.
  RM   90085815
  RA   PARKER S.E., GALLAGHER T.M., BUCHMEIER M.J.;
  RL   VIROLOGY 173:664-673(1989).
  CC   -!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
  CC       TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
  CC   -!- SIMILARITY: NEARLY IDENTICAL TO THE E2 GLYCOPROTEINS FROM MVH-JHM
  CC       AND MVH-A59 STRAINS, EXCEPT FOR AN N-TERMINAL INSERTION.
  CC   -!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE GLYCOPROTEIN.
  DR   EMBL; M32799; MHVE2GLY.
  DR   PIR; A33748; VGIHJ2.
  KW   GLYCOPROTEIN; ENVELOPE PROTEIN; TRANSMEMBRANE; SIGNAL.
  FT   SIGNAL          1     14
```

FT	CHAIN	770	1376	SPIKE PROTEIN S1 (90K).
FT	DOMAIN	15	1320	SPIKE PROTEIN S2 (90A).
FT	TRANSMEM	1321	1338	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	1339	1376	POTENTIAL.
FT	DOMAIN	429	599	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	31	31	IMPORTANT FOR THE NEUROVIRULENCE.
FT	CARBOHYD	60	60	POTENTIAL.
FT	CARBOHYD	134	134	POTENTIAL.
FT	CARBOHYD	192	192	POTENTIAL.
FT	CARBOHYD	357	357	POTENTIAL.
FT	CARBOHYD	435	435	POTENTIAL.
FT	CARBOHYD	582	582	POTENTIAL.
FT	CARBOHYD	677	677	POTENTIAL.
FT	CARBOHYD	709	709	POTENTIAL.
FT	CARBOHYD	717	717	POTENTIAL.
FT	CARBOHYD	740	740	POTENTIAL.
FT	CARBOHYD	789	789	POTENTIAL.
FT	CARBOHYD	806	806	POTENTIAL.
FT	CARBOHYD	945	945	POTENTIAL.
FT	CARBOHYD	1232	1232	POTENTIAL.
FT	CARBOHYD	1242	1242	POTENTIAL.
FT	CARBOHYD	1261	1261	POTENTIAL.
FT	CARBOHYD	1277	1277	POTENTIAL.
FT	CARBOHYD	1298	1298	POTENTIAL.
FT	CARBOHYD	1370	1370	POTENTIAL.
SQ	SEQUENCE	1376 AA;	151882 MW;	9626615 CN;
CC	-!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB			

Initial Score	=	5	Optimized Score	=	5	Significance	= 0.00
Residue Identity	=	100%	Matches	=	5	Mismatches	= 0
Gaps	=	0	Conservative Substitutions				= 0

```
                                                                  X    X
                                                                  YLNAT
                                                                  |||||
    MLFVFILLLPSCLGYIGDFRCI@TVNYNGNNASAPSISTEAVDVSKGLGTYYVLDRVYLNATLLLTGYYPVD
            10        20        30        40        50        60 X      70

    GSNYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKV@NLKTNTPTGATSYFPTIVIGSLFGNTSYTVVLEPY
          80        90        100       110       120       130       140

    NNIIMASVCTYTIC@LPY
       150       160
```

14. CELSA-14 (1-5)

VGIH59 E2 glycoprotein precursor - Murine hepatitis virus

ENTRY	VGIH59 #Type Protein
TITLE	E2 glycoprotein precursor - Murine hepatitis virus (strain A59)
ALTERNATE-NAME	peplomer glycoprotein\ spike glycoprotein
DATE	31-Mar-1989 #Sequence 31-Mar-1989 #Text 30-Sep-1992
PLACEMENT	2231.0 4.0 1.0 1.0 1.0
SOURCE	murine hepatitis virus, MHV
ACCESSION	A27402
REFERENCE	
#Authors	Luytjes W., Sturman L.S., Bredenbeek P.J., Charite J., van der Zeijst B.A.M., Horzinek M.C., Spaan W.J.M.
#Journal	Virology (1987) 161:479-487
#Title	Primary structure of the glycoprotein E2 of [illegible]

```
    #Molecule-type genomic RNA
    #Residues      1-1324 <LUY>
 COMMENT           This virus is a member of the family Coronaviridae.
 SUPERFAMILY       #Name coronavirus E2 glycoprotein
 KEYWORDS          glycoprotein
 FEATURE
    1-16                          #Domain signal sequence <SIG>\
    17-1324                       #Protein E2 glycoprotein <E2G>\
    17-717                        #Protein 90B glycoprotein <EGB>\
    718-1324                      #Protein 90A glycoprotein <EGA>\
    31,60,192,247,357,435,
    442,530,625,657,665,
    688,737,754,844,893,
    1126,1180,1190,1209,
    1225,1246,1318                #Binding-site carbohydrate (Asn)
                                    (covalent) (predicted)\
    1266-1286                     #Domain transmembrane <TMN>
 SUMMARY      #Molecular-weight 145963  #Length 1324  #Checksum  7500
 SEQUENCE
 COMMENT           Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0

                                                                  X    X
                                                                  YLNAT
                                                                  |||||
    MLFVFILFLPSCLGYIGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYYVLDRVYLNATLLLTGYYPVD
            10        20        30        40        50        60 X      70

    GSKFRNLALTGTNSVSLSWFQPPYLNQFNDGIFAKVQNLKTSTPSGATAYFPTIVIGSLFGYTSYTVVIEPY
          80        90        100       110       120       130       140

    NGVIMASVCQYTICQLPY
       150       160


15. CELSA-14 (1-5)
    VGL2_CVMA5   E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PE

 ID   VGL2_CVMA5     STANDARD;      PRT;  1324 AA.
 AC   P11224;
 DT   01-JUL-1989 (REL. 11, CREATED)
 DT   01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT   01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE   E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).
 GN   S.
 OS   MURINE CORONAVIRUS MHV (STRAIN A59).
 OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; CORONAVIRIDAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   88072088
 RA   LUYTJES W., STURMAN L.S., BREDENBEEK P.J., CHARITE J.,
 RA   VAN DER ZEIJST B.A.M., HORZINEK M.C., SPAAN W.J.M.;
 RL   VIROLOGY 161:479-487(1987).
 CC   -!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
 CC       TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
 CC   -!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE GLYCOPROTEIN.
 DR   EMBL; M18379; CORMHVE2.
 DR   PIR; A27402; VGIH59.
 KW   GLYCOPROTEIN; ENVELOPE PROTEIN, TRANSMEMBRANE; SIGNAL
 FT   SIGNAL          1     16
 FT   CHAIN           17    1324                    .....
```

```
FT   DOMAIN       718   1324        SPIKE PROTEIN S2 (90A).
FT   DOMAIN        17   1265        EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    1266   1286
FT   DOMAIN      1287   1324        CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      31     31        POTENTIAL.
FT   CARBOHYD      60     60        POTENTIAL.
FT   CARBOHYD     192    192        POTENTIAL.
FT   CARBOHYD     357    357        POTENTIAL.
FT   CARBOHYD     435    435        POTENTIAL.
FT   CARBOHYD     530    530        POTENTIAL.
FT   CARBOHYD     625    625        POTENTIAL.
FT   CARBOHYD     657    657        POTENTIAL.
FT   CARBOHYD     665    665        POTENTIAL.
FT   CARBOHYD     688    688        POTENTIAL.
FT   CARBOHYD     737    737        POTENTIAL.
FT   CARBOHYD     754    754        POTENTIAL.
FT   CARBOHYD     893    893        POTENTIAL.
FT   CARBOHYD    1180   1180        POTENTIAL.
FT   CARBOHYD    1190   1190        POTENTIAL.
FT   CARBOHYD    1209   1209        POTENTIAL.
FT   CARBOHYD    1225   1225        POTENTIAL.
FT   CARBOHYD    1246   1246        POTENTIAL.
FT   CARBOHYD    1318   1318        POTENTIAL.
SQ   SEQUENCE   1324 AA;  145964 MW;  9039956 CN;
CC   -!- Retrieved by alexk on Thu 25 Feb 93 10:29:02-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0

                                                                  X    X
                                                                  YLNAT
                                                                  |||||
   MLFVFILFLPSCLGYIGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYYVLDRVYLNATLLLTGYYPVD
            10         20         30         40         50         60 X       70

   GSKFRNLALTGTNSVSLSWFQPPYLNQFNDGIFAKVQNLKTSTPSGATAYFPTIVIGSLFGYTSYTVVIEPY
         80         90        100        110        120        130        140

   NGVIMASVCQYTICQLPY
      150        160


16. CELSA-14 (1-5)
    VGIHMJ        E2 glycoprotein precursor - Murine hepatitis virus

 ENTRY            VGIHMJ      #Type Protein
 TITLE            E2 glycoprotein precursor - Murine hepatitis virus
                    (strain JHM)
 ALTERNATE-NAME   peplomer glycoprotein\ spike glycoprotein
 INCLUDES         90B glycoprotein\ 90A glycoprotein
 DATE             31-Mar-1991 #Sequence 31-Mar-1991 #Text 30-Sep-1992
 PLACEMENT        2231.0     4.0     1.0     2.0     1.0
 SOURCE           murine hepatitis virus, MHV
 ACCESSION        A33095
 REFERENCE
    #Authors      Schmidt I.; Skinner M.; Siddell S.
    #Journal      J. Gen. Virol. (1987) 68:47-56
    #Title        Nucleotide sequence of the gene encoding the surface
                   projection glycoprotein of coronavirus MHV-JHM.
    #Reference-number A33095
    #Accession    A33095
    #Molecule-type genomic RNA
    #Residues     1-1324 <SCH>
 COMMENT
```

```
                glycoprotein; membrane protein
FEATURE
     1-10                    #Domain signal sequence <SIG>\
     11-1235                 #Protein E2 glycoprotein <E2G>\
     11-628                  #Protein 90B glycoprotein <EGB>\
     629-1235                #Protein 90A glycoprotein <EGA>\
     1175-1208               #Domain transmembrane <TMN>\
     31,60,134,192,357,435,
     442,536,568,576,599,
     648,665,755,804,1037,
     1091,1101,1120,1136,
     1157,1229
                             #Binding-site carbohydrate (Asn)
                               (covalent) (predicted)
SUMMARY      #Molecular-weight 136653  #Length 1235  #Checksum  9154
SEQUENCE
COMMENT          Retrieved by alexk on Thu 25 Feb 93 10:29:03-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0


                                                                  X    X
                                                                  YLNAT
                                                                  |||||
    MLFVFILLLPSCLGYIGDFRCIQTVNYNGNNASAPSISTEAVDVSKGRGTYYVLDRVYLNATLLLTGYYPVD
            10        20        30        40        50        60 X      70

    GSNYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKVQNLKTNTPTGATSYFPTIVIGSLFGNTSYTVVLEPY
          80        90        100       110       120       130       140

    NNIIMASVCTYTICQLPY
       150       160


17. CELSA-14 (1-5)
    VGL2_CVMJH   E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PE

ID   VGL2_CVMJH     STANDARD;      PRT;  1235 AA.
AC   P11225;
DT   01-JUL-1989 (REL. 11, CREATED)
DT   01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT   01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
DE   E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).
GN   S.
OS   MURINE CORONAVIRUS MHV (STRAIN JHM).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; CORONAVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   87111467
RA   SCHMIDT I., SKINNER M.A., SIDDELL S.G.;
RL   J. GEN. VIROL. 68:47-56(1987).
CC   -!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
CC       TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
CC   -!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE GLYCOPROTEIN.
DR   EMBL; X04797; COMHVS.
DR   PIR; A33095; VGIHMJ.
KW   GLYCOPROTEIN; ENVELOPE PROTEIN; TRANSMEMBRANE; SIGNAL.
FT   SIGNAL          1     19        POTENTIAL.
FT   CHAIN          11   1235        SPIKE E2 GLYCOPROTEIN.
FT   CHAIN          11    628        SPIKE PROTEIN S1 (90B).
FT   CHAIN         629   1235        SPIKE PROTEIN S2 (90A).
FT   DOMAIN         11   1174        EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     1175   1208        POTENTIAL.
FT   DOMAIN       1209   1235        CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD       31     31
```

```
FT    CARBOHYD     192     192          POTENTIAL.
FT    CARBOHYD     357     357          POTENTIAL.
FT    CARBOHYD     435     435          POTENTIAL.
FT    CARBOHYD     536     536          POTENTIAL.
FT    CARBOHYD     568     568          POTENTIAL.
FT    CARBOHYD     576     576          POTENTIAL.
FT    CARBOHYD     599     599          POTENTIAL.
FT    CARBOHYD     648     648          POTENTIAL.
FT    CARBOHYD     665     665          POTENTIAL.
FT    CARBOHYD     804     804          POTENTIAL.
FT    CARBOHYD    1091    1091          POTENTIAL.
FT    CARBOHYD    1101    1101          POTENTIAL.
FT    CARBOHYD    1120    1120          POTENTIAL.
FT    CARBOHYD    1136    1136          POTENTIAL.
FT    CARBOHYD    1157    1157          POTENTIAL.
FT    CARBOHYD    1229    1229          POTENTIAL.
SQ    SEQUENCE   1235 AA;  136653 MW;  7753984 CN;
CC    -!- Retrieved by alexk on Thu 25 Feb 93 10:29:03-PST using FastDB

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0

                                                                  X    X
                                                                  YLNAT
                                                                  |||||
    MLFVFILLLPSCLGYIGDFRCI@TVNYNGNNASAPSISTEAVDVSKGRGTYYVLDRVYLNATLLLTGYYPVD
              10        20        30        40        50        60 X      70

    GSNYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKV@NLKTNTPTGATSYFPTIVIGSLFGNTSYTVVLEPY
          80        90        100       110       120       130       140

    NNIIMASVCTYTIC@LPY
       150       160


18. CELSA-14 (1-5)
    A40986          *M-cadherin - Mouse (fragment)

ENTRY               A40986      *Type Protein (fragment)
TITLE               *M-cadherin - Mouse (fragment)
DATE                16-Apr-1992 *Sequence 16-Apr-1992 *Text 16-Apr-1992
PLACEMENT              0.0     0.0     0.0     0.0     0.0
COMMENT             *This entry is not verified.
SOURCE              Mus musculus *Common-name house mouse
REFERENCE
    *Authors        Donalies M., Cramer M., Ringwald M.,
                      Starzinski-Powitz A.
    *Journal        Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8024-8028
    *Title          Expression of M-cadherin, a member of the cadherin
                      multigene family, correlates with differentiation
                      of skeletal muscle cells.
    *Reference-number A40986
    *Accession      A40986
    *Cross-reference GB:M74541
SUMMARY
SEQUENCE                                    *Length 770  *Checksum  4192
COMMENT             Retrieved by alexk on Thu 25 Feb 93 [illegible]

Initial Score     =       5  Optimized Score  =       5  Significance =   0.00
Residue Identity  =    100%  Matches          =       5  Mismatches   =      0
Gaps              =       0  Conservative Substitutions                =      0
```

```
ENHKRLPYPLVQIKSDKQQLGSVIYSIQGPGVDEEPRNVFSIDKFTGRVYLNATLDRETKDRFRLRAFALDL
        10        20        30        40        50   X    60        70

GGSTLEDPTDLEIVVVDQNDNRPAFLQDVFRGHILEGAIPGTFVTRAEATDADDPETDNAALRFSILEQGSP
      80        90       100       110       120       130       140

EFFSIDEHTG
   150
```

19. CELSA-14 (1-5)
SAHU4F Cell surface antigen 4F2 heavy chain - Human

ENTRY SAHU4F #Type Protein
TITLE Cell surface antigen 4F2 heavy chain - Human
DATE 30-Jun-1990 #Sequence 30-Jun-1990 #Text 30-Jun-1992
PLACEMENT 962.0 1.0 1.0 1.0 1.0
SOURCE Homo sapiens #Common-name man
ACCESSION A28455\ A28314\ A30240
REFERENCE
#Authors Teixeira S., Di Grandi S., Kuehn L.C.
#Journal J. Biol. Chem. (1987) 262:9574-9580
#Title Primary structure of the human 4F2 antigen heavy chain predicts a transmembrane protein with a cytoplasmic NH2 terminus.
#Reference-number A28455
#Accession A28455
#Molecule-type mRNA
#Residues 1-529 <TEI>
REFERENCE
#Authors Quackenbush E., Clabby M., Gottesdiener K.M., Barbosa J., Jones N.H., Strominger J.L., Speck S., Leiden J.M.
#Journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6526-6530
#Title Molecular cloning of complementary DNAs encoding the heavy chain of the human 4F2 cell-surface antigen: a type II membrane glycoprotein involved in normal and neoplastic cell growth.
#Reference-number A28314
#Accession A28314
#Molecule-type mRNA
#Residues 1-529 <QUA>
#Comment The authors' translation, given in Fig. 5, is missing residues 92-94, while the nucleotide sequence is missing the codons for residues 121-123. Consequently, the codons for residues 92-120 are associated with the translation corresponding to residues 95-123.
REFERENCE
#Authors Gottesdiener K.M., Karpinski B.A., Lindsten T., Strominger J.L., Jones N.H., Thompson C.B., Leiden J.M.
#Journal Mol. Cell. Biol. (1988) 8:3809-3819
#Title Isolation and structural characterization of the human 4F2 heavy-chain gene, an inducible gene involved in T-lymphocyte activation.
#Reference-number A30240
#Accession A30240
#Molecule-type DNA
#Residues 1-529 <GOT>
#Comment The nucleotide sequence in Fig. 1 is inconsistent with the authors' translation in having the codon TTC (Phe) for Ser-212 and GAA (Glu) for Lys-401.

proliferating and transformed cells. It may be involved in the regulation of intracellular calcium concentration and the concomitant control of growth, excitability, and endocrine secretion.

COMMENT The molecule is a heterodimer consisting of a glycosylated heavy chain and a nonglycosylated light chain linked by at least one disulfide bond.

GENETIC
*Map-position 11q
*Name MDU1
*Introns 142/1, 200/1, 230/3, 253/3, 273/2, 333/3, 381/3, 409/3

SUPERFAMILY *Name cell surface antigen 4F2 heavy chain
KEYWORDS glycoprotein\ heterodimer\ surface antigen\ transmembrane protein

FEATURE
1-81 *Domain cytoplasmic <CYT>\
82-104 *Domain transmembrane <TMN>\
105-529 *Domain extracellular <EXT>\
264,280,323,405 *Binding-site carbohydrate (Asn) (covalent) (predicted)

SUMMARY *Molecular-weight 57944 *Length 529 *Checksum 8988
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 10:29:03-PST using FastDB

Initial Score = 5 Optimized Score = 5 Significance = 0.00
Residue Identity = 100% Matches = 5 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
QVDTVATKVKDALEFWLQAGVDGFQVRDIENLKDASSFLAEWQNITKGFSEDRLLIAGTNSSDLQQILSLLE
      230       240       250       260       270       280       290

                                X   X
                                YLNAT
                                |||||
SNKDLLLLTSSYLSDSGSTGEHTKSLVTQYLNATGNRWCSWSLSQARLLTSFLPAQLLRLYQLMLFTLPGTPV
     300       310       320    X  330       340       350       360

FSYGDEIGLDAAALPGQPMEAPVMLWDESSFPDIPGAVSANMTVKGQSEDPGSLLSLFRRL
   370       380       390       400       410       420
```

20. CELSA-14 (1-5)
A39984 *Cell surface antigen 4F2 heavy chain - Human

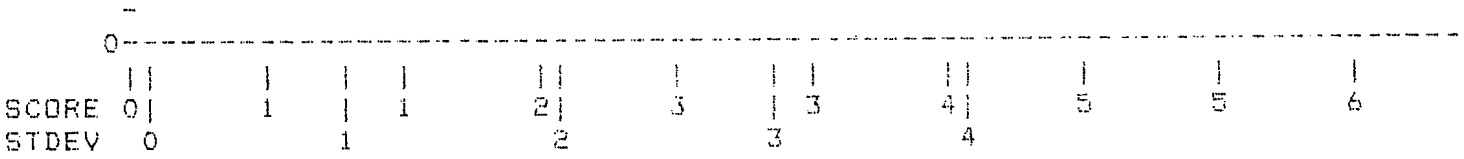
ENTRY A39984 *Type Protein
TITLE *Cell surface antigen 4F2 heavy chain - Human
DATE 24-Jan-1992 *Sequence 24-Jan-1992 *Text 21-Jan-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
COMMENT *This entry is not verified.
SOURCE Homo sapiens *Common-name man
REFERENCE
*Authors Quackenbush E., Clabby M., Gottesdiener K.M., Barbosa J., Jones N.H., Strominger J.L., Speck S., Leiden J.M.
*Journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6858
*Reference-number A39984
*Accession A39984
SUMMARY *Molecular-weight 57913 *Length 529 [illegible]
SEQUENCE
COMMENT Retrieved by alexk on Thu 25 Feb 93 [illegible] using FastDB

Initial Score = [illegible] Optimized Score = [illegible] Significance = [illegible]
Residue Identity = [illegible] Matches = [illegible] Mismatches = [illegible]
Gaps = [illegible] Conservative Substitutions = [illegible]

```
QVDTVATKVKDALEFWLQAGVQGFQVRDIENLKDAGSFLAEWQNITKQFSEDRLLIAGTNSSDLQQILSLLE
       230       240       250       260       270       280       290

                                  X    X
                                  YLNAT
                                  |||||
SNKDLLLTSSYLSDSCSTGEHTKSLVTQYLNATGNRWCSWSLSQARLLTSFLFAQLLRLYQLMLFTLPGTFV
      300       310       320     X 330       340       350       360

FSYGDEIGLDAAALPGQPMEAPVMLWDESSFPDIPGAVSANMTVKGQSEDPGSLLSLFRRL
    370       380       390       400       410       420
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.08

Times:	CPU	Total Elapsed
	00:03:20.10	00:07:11.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4353

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

see next printout for alignments

4 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	POLG_TBEVW	GENOME POLYPROTEIN (CONTAINS:	3414	6	6	4.63	0
2.	GNWVNE	Genome polyprotein - Tick-bor	3414	6	6	4.63	0
3.	GNWVTB	Genome polyprotein - Tick-bor	3412	6	6	4.63	0
4.	POLG_TBEVS	GENOME POLYPROTEIN (CONTAINS:	3412	6	6	4.63	0

The list of other best scores is:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 3 standard deviations above [illegible] ****					
5.	CBPC_HUMAN	MAST CELL CARBOXYPEPTIDASE A	417	3	3	3.70	0
6.	A39246	*Carboxypeptidase A precursor	417	3	3	3.70	0
7.	S04912	mycpA protein - Yersinia ente	403	3	3	3.70	0
8.	PT2S_UACSU	PHOSPHOTRANSFERASE ENZYME II,	450	3	3	3.70	0
9.	A37933	*Phosphotransferase system [illegible]	450	3	3	3.70	0
10.	KR2_HUMAN	KRAB-A DOMAIN-CONTAINING ZINC	400	3	3	3.70	0
11.	B50093	[illegible]	450	3	3	3.70	0

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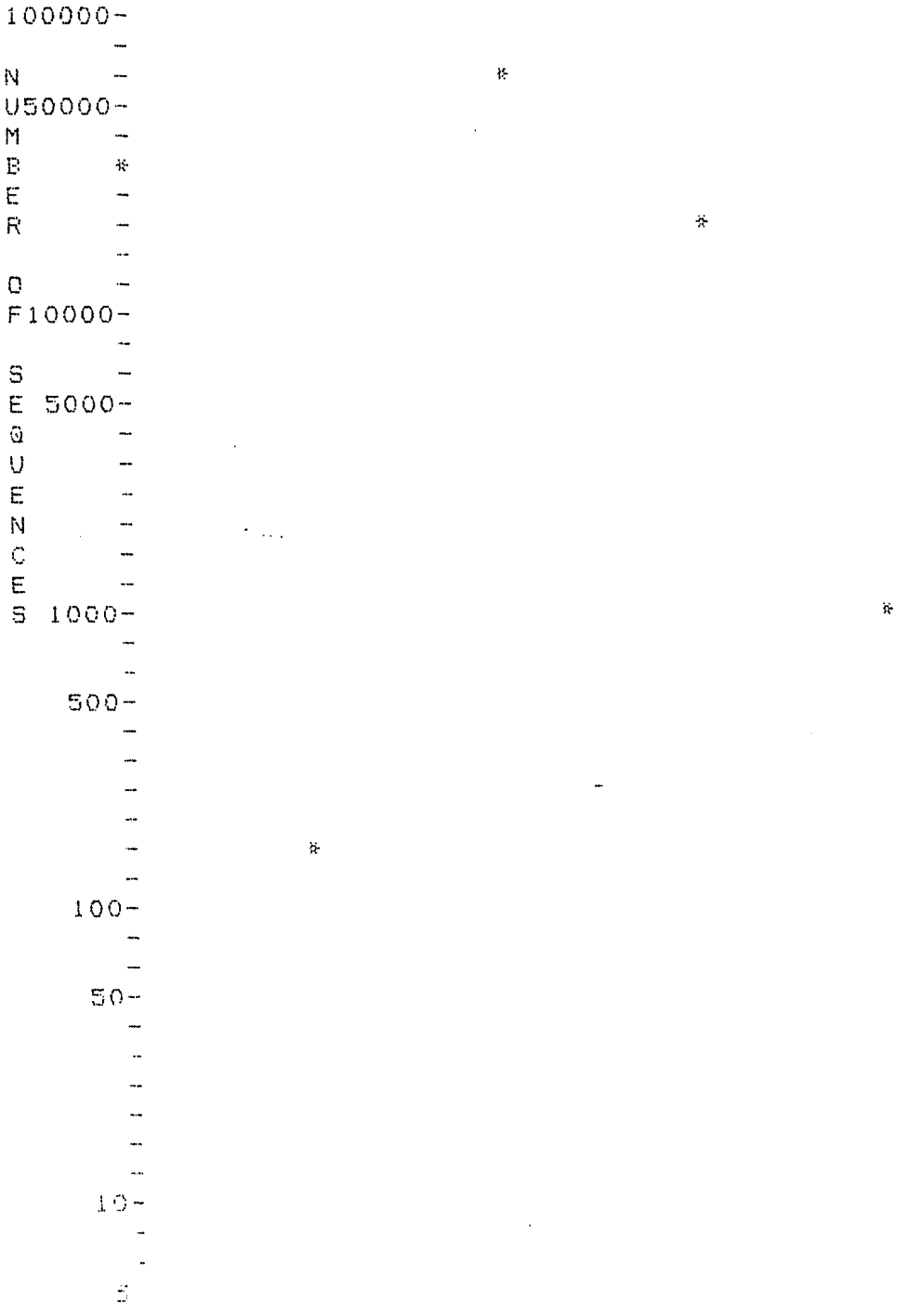
Sequences numbered as in table 4 1-19 (not by seq ID #)

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-1.res made by alexk on Thu 25 Feb 93 10:21:13-PST.

Query sequence being compared: CELSA-1 (1-6)
Number of sequences searched: 94553
Number of scores above cutoff: 4353

'Results of the initial comparison of CELSA-1 (1-6) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries



14. DNBI_HSV1F	MAJOR DNA-BINDING PROTEIN.	1196	5	5	3.70	0
15. DNBI_HSV11	MAJOR DNA-BINDING PROTEIN.	1196	5	5	3.70	0
16. B30085	*Gene UL29 protein (major DNA	1196	5	5	3.70	0
17. DNBEHF	DNA-binding protein - Human h	1196	5	5	3.70	0
18. DNBEKS	DNA-binding protein - Human h	1196	5	5	3.70	0
19. DNBEV1	DNA-binding protein - Human h	1196	5	5	3.70	0
20. S19926	*Hypothetical protein - Red c	1864	5	5	3.70	0
	**** 2 standard deviations above mean ****					
21. A36696	*Tumor necrosis factor - Mous	20	4	4	2.78	0
22. P50250	N-terminal of cytotatic prot	27	4	4	2.78	0
23. P98441	Sequence of C. trachomatis se	31	4	4	2.78	0
24. VG5_BPPH2	PROBABLE EARLY PROTEIN GP5.	66	4	4	2.78	0
25. ERBP59	Early protein gp5 (version 1)	66	4	4	2.78	0
26. A41608	*Hypothetical protein 1 - Rho	68	4	4	2.78	0
27. C552_BRAJA	CYTOCHROME C552.	73	4	4	2.78	0
28. PRT2_SEPOF	SPERMATID-SPECIFIC PROTEIN T2	77	4	4	2.78	0
29. B40973	*Spermatid-specific protein T	77	4	4	2.78	0
30. A27120	Epidermal growth factor-bindi	77	4	4	2.78	0
31. PRT1_SEPOF	SPERMATID-SPECIFIC PROTEIN T1	78	4	4	2.78	0
32. A40973	*Spermatid-specific protein T	78	4	4	2.78	0
33. HPIS_THIRO	HIGH POTENTIAL IRON-SULFUR PR	85	4	4	2.78	0
34. IHTFER	High potential iron-sulfur pr	85	4	4	2.78	0
35. P60677	Human seminal alpha-inhibin-5	92	4	4	2.78	0
36. S11892	*Hypothetical protein - Fruit	95	4	4	2.78	0
37. S18821	*Cytochrome c552 - Bradyrhizo	104	4	4	2.78	0
38. APL1_PETMA	BLOOD PLASMA APOLIPOPROTEIN L	105	4	4	2.78	0
39. A26602	Apolipoprotein 1 precursor -	105	4	4	2.78	0
40. CUP4_DROME	LARVAL CUTICLE PROTEIN IV PRE	112	4	4	2.78	0
41. CUP3_DROME	LARVAL CUTICLE PROTEIN III PR	112	4	4	2.78	0
42. D25299	Cuticle protein IV precursor	112	4	4	2.78	0
43. C25299	Cuticle protein III precursor	112	4	4	2.78	0
44. R10046	Region of IBDV strain E contg	113	4	4	2.78	0
45. MOTI_HUMAN	MOTILIN PRECURSOR.	115	4	4	2.78	0
46. A33323	*Promotilin precursor - Human	115	4	4	2.78	0
47. S04489	*Motilin - Human	115	4	4	2.78	0
48. S00156	Motilin precursor - Human	115	4	4	2.78	0
49. P80459	Sequence corresp. to the nucl	115	4	4	2.78	0
50. PA2_NAJPA	PHOSPHOLIPASE A2 (EC 3.1.1.4)	118	4	4	2.78	0

No alignments saved.

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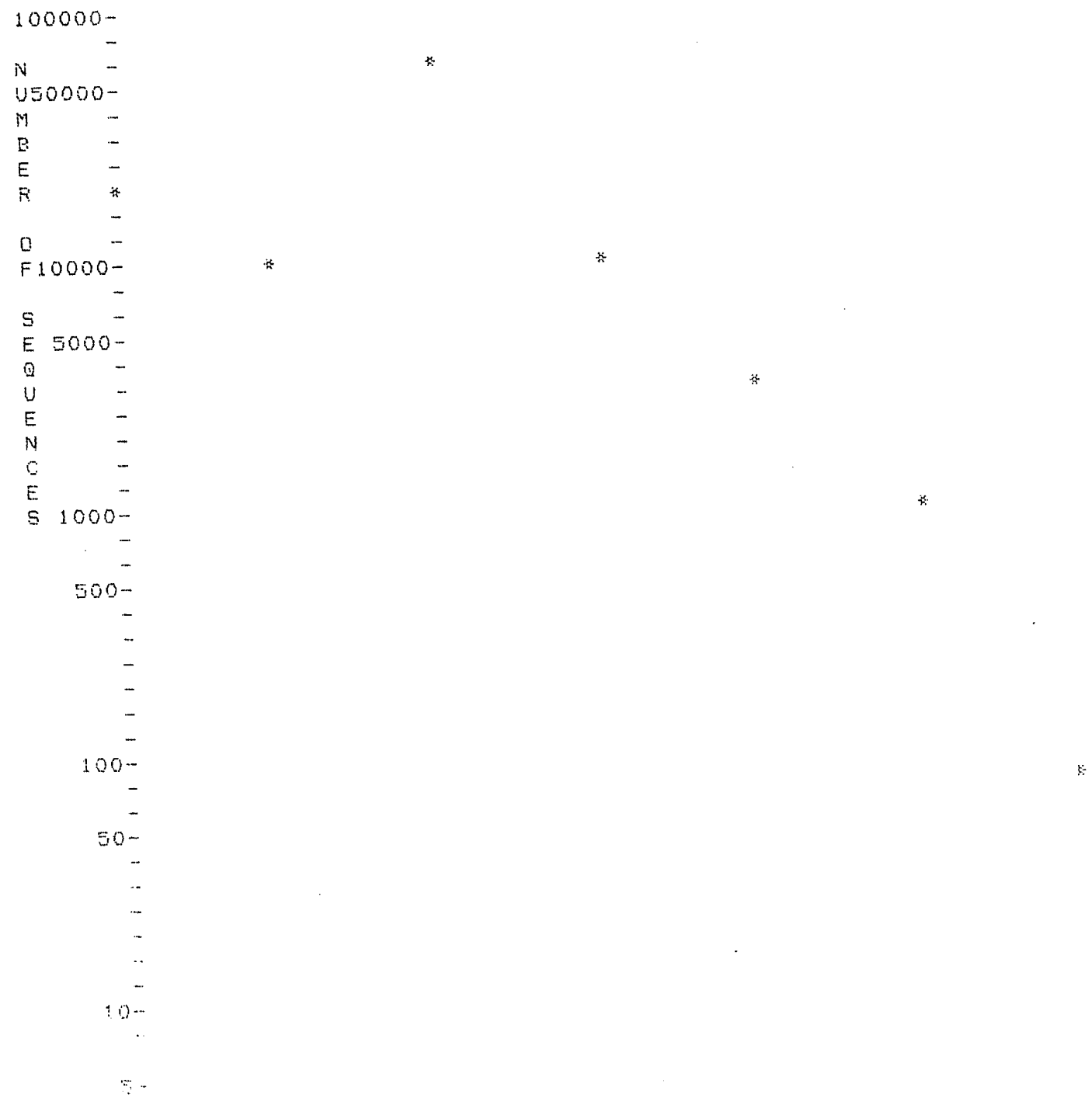
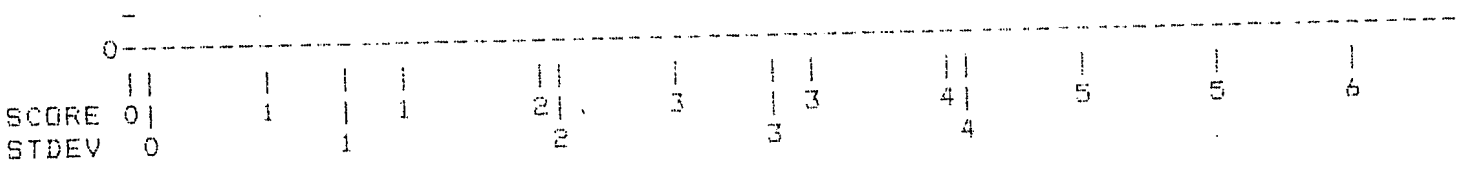
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-2.res made by alexk on Thu 25 Feb 93 10:37:07-PST.

Query sequence being compared: CELSA-2 (1-7)
Number of sequences searched: 94553
Number of scores above cutoff: 4289

Results of the initial comparison of CELSA-2 (1-7) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	1	3	1.06

	CPU	Total Elapsed
Times:	00:03:25.08	00:07:03.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4289

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 4 standard deviations above mean ****					
1. YXYB_CALSA	HYPOTHETICAL 10.7 KD PROTEIN	97	6	6	4.73	0
2. C37202	*Hypothetical protein, XynC 3	97	6	6	4.73	0
3. R05567	Plant elongation factor-1 alp	293	6	6	4.73	0
4. R05569	Plant elongation factor-1 alp	294	6	6	4.73	0
5. ADT1_YEAST	ADP,ATP CARRIER PROTEIN 1 (AD	309	6	6	4.73	0
6. A24849	ADP,ATP carrier protein AAC1	309	6	6	4.73	0
7. S13805	*Elongation factor eEF-1 alph	323	6	6	4.73	0
8. A37159	*Centrosphere protein, elonga	325	6	6	4.73	0
9. A29946	Elongation factor 1 alpha cha	327	6	6	4.73	0
10. EF1A_RHYAM	ELONGATION FACTOR 1-ALPHA (EF	412	6	6	4.73	0
11. EF1A_EUGGR	ELONGATION FACTOR 1-ALPHA (EF	445	6	6	4.73	0
12. S07724	*Elongation factor eEF-1 alph	445	6	6	4.73	0
13. EF1A_STYLE	ELONGATION FACTOR 1-ALPHA (EF	446	6	6	4.73	0
14. S16308	*Elongation factor eEF-1 alph	447	6	6	4.73	0

17.	JS0719	Elongation factor 1 alpha cha	447	6	6	4.73	0
18.	EF1A_LYCES	ELONGATION FACTOR 1-ALPHA (EF	448	6	6	4.73	0
19.	S10507	*Elongation factor eEF-1 alph	448	6	6	4.73	0
20.	S09355	*Elongation factor eEF-1 alph	448	6	6	4.73	0
21.	R05565	Plant elongation factor-1 alp	448	6	6	4.73	0
22.	EF1A_ARATH	ELONGATION FACTOR 1-ALPHA (EF	449	6	6	4.73	0
23.	S21989	*Elongation factor 1A - Carro	449	6	6	4.73	0
24.	S08348	*Elongation factor eEF-1 alph	449	6	6	4.73	0
25.	S08534	*Elongation factor eEF-1 alph	449	6	6	4.73	0
26.	A32684	Elongation factor 1 alpha cha	449	6	6	4.73	0
27.	S06724	Elongation factor 1 alpha cha	449	6	6	4.73	0
28.	S10226	*Elongation factor eEF-1 alph	454	6	6	4.73	0
29.	EF1A_DICDI	ELONGATION FACTOR 1-ALPHA (EF	456	6	6	4.73	0
30.	S11665	*Elongation factor eEF-1 alph	456	6	6	4.73	0
31.	EF13_RHIRA	ELONGATION FACTOR 1-ALPHA (EF	457	6	6	4.73	0
32.	EF1A_YEAST	ELONGATION FACTOR 1-ALPHA (EF	458	6	6	4.73	0
33.	EF1A_CANAL	ELONGATION FACTOR 1-ALPHA (EF	458	6	6	4.73	0
34.	EF12_RHIRA	ELONGATION FACTOR 1-ALPHA (EF	458	6	6	4.73	0
35.	EF11_RHIRA	ELONGATION FACTOR 1-ALPHA (EF	458	6	6	4.73	0
36.	A35154	*Elongation factor 1 alpha -	458	6	6	4.73	0
37.	A25938	Elongation factor 1 alpha cha	458	6	6	4.73	0
38.	S08058	Elongation factor 1 alpha-3 c	458	6	6	4.73	0
39.	S06300	Elongation factor 1 alpha-2 c	458	6	6	4.73	0
40.	EFBY1A	Elongation factor eEF-1 alpha	458	6	6	4.73	0
41.	EF1A_MOUSE	ELONGATION FACTOR 1-ALPHA (EF	461	6	6	4.73	0
42.	EF1A_ARTSA	ELONGATION FACTOR 1-ALPHA (EF	461	6	6	4.73	0
43.	EF1A_APIME	ELONGATION FACTOR 1-ALPHA (EF	461	6	6	4.73	0
44.	EF13_XENLA	ELONGATION FACTOR 1-ALPHA, OO	461	6	6	4.73	0
45.	EF12_XENLA	ELONGATION FACTOR 1-ALPHA, OO	461	6	6	4.73	0
46.	S13806	*Elongation factor eEF-1 alph	461	6	6	4.73	0
47.	S10225	*Elongation factor eEF-1 alph	461	6	6	4.73	0
48.	JH0530	Elongation factor 1-alpha O -	461	6	6	4.73	0
49.	EFHB1	Elongation factor eEF-1 alpha	461	6	6	4.73	0
50.	EFMS1	Elongation factor eEF-1 alpha	461	6	6	4.73	0

No alignments saved.

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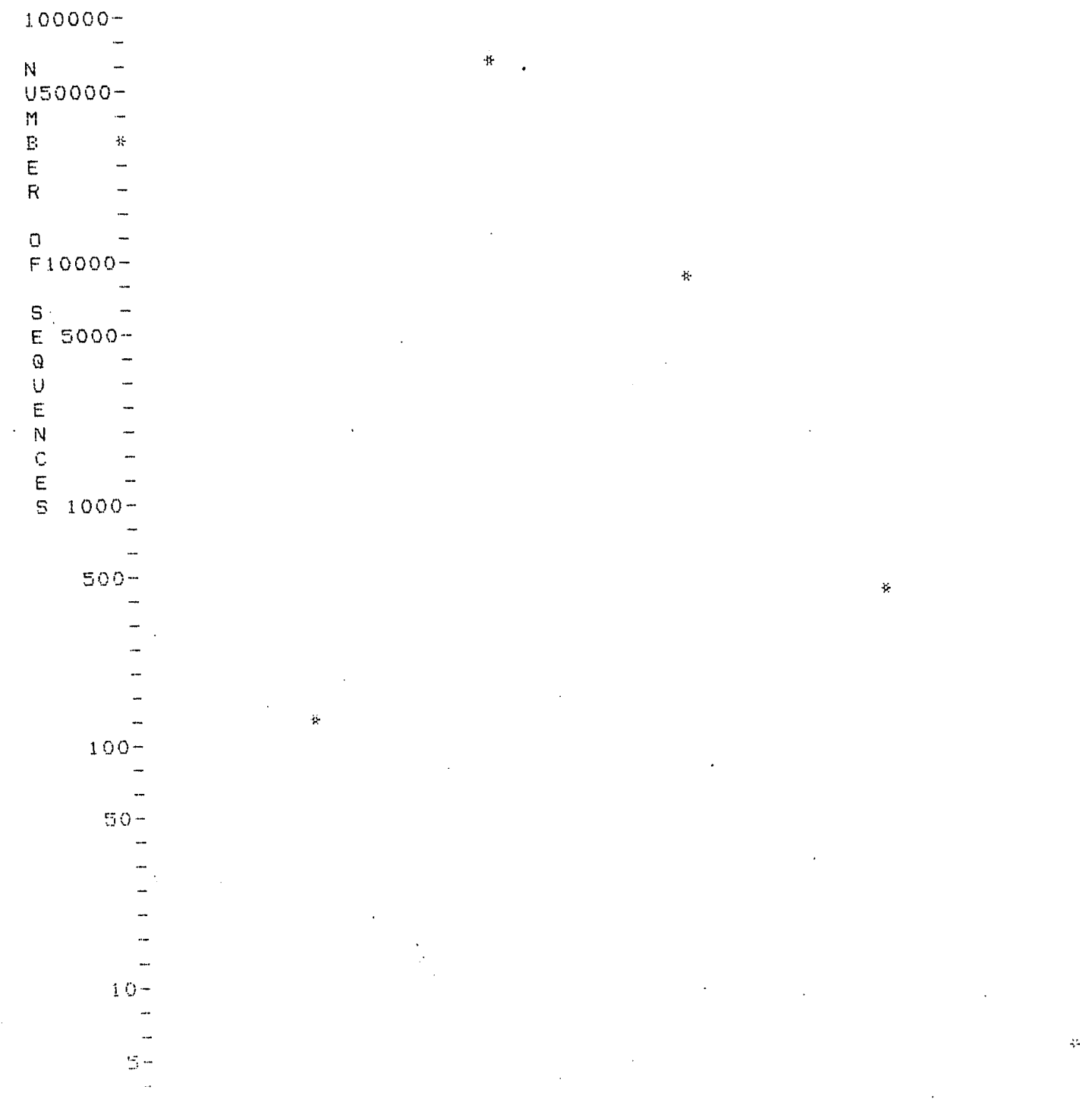
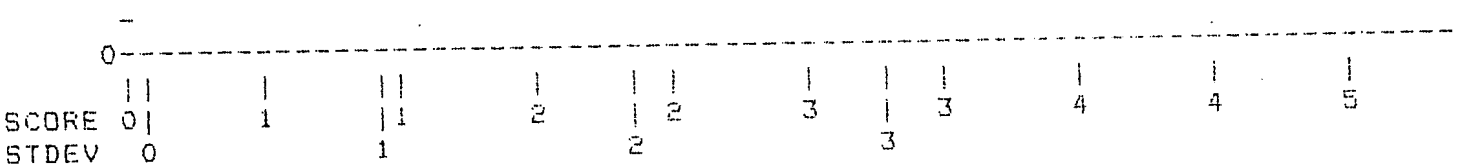
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-3.res made by alexk on Thu 25 Feb 93 10:28:59-PST.

Query sequence being compared: CELSA-3 (1-5)
Number of sequences searched: 94553
Number of scores above cutoff: 4004

Results of the initial comparison of CELSA-3 (1-5) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.03

Times:	CPU	Total Elapsed
	00:03:18.96	00:06:54.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4004

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

5 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. PULA_KLEAE	PULLULANASE (EC 3.2.1.41) (AL	1096	5	5	3.89	0
2. A26879	alpha-Dextrin endo-1,6-alpha-	1096	5	5	3.89	0
3. P82507	Pullulanase protein.	1096	5	5	3.89	0
4. DBH_THETH	DNA-BINDING PROTEIN II.	95	5	5	3.89	0
5. S12888	*DNA-binding protein II - The	95	5	5	3.89	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
6. S10561	*Photosystem II 21K protein -	56	4	4	2.92	0
7. C551_PSEST	CYTOCHROME C551.	82	4	4	2.92	0
8. CCPS5S	Cytochrome c551 - Pseudomonas	83	4	4	2.92	0
9. CYC6_PLEBO	CYTOCHROME C6 (SOLUBLE CYTOCH	84	4	4	2.92	0
10. CCPB6	Cytochrome c6 - Plectonema bo	85	4	4	2.92	0
11. CYC6_ANAVA	CYTOCHROME C6 (SOLUBLE CYTOCH	89	4	4	2.92	0

14.	DNBS2F	DNA-binding protein II - Bacl	92	4	4	2.92	0
15.	DBH_BACSU	DNA-BINDING PROTEIN II (HB) (	92	4	4	2.92	0
16.	B39409	*DNA-binding protein HB - Bac	92	4	4	2.92	0
17.	S00015	DNA-binding protein HB - Baci	104	4	4	2.92	0
18.	R05446	CAT-GLP-1 hybrid protein.	105	4	4	2.92	0
19.	PINO_ECOLI	PINO PROTEIN.	105	4	4	2.92	0
20.	GLN1_METTL	NITROGEN FIXATION NIFHD REGIO	105	4	4	2.92	0
21.	S08095	*Hypothetical protein (nifH1	105	4	4	2.92	0
22.	S06985	Hypothetical protein (nifH1 3	105	4	4	2.92	0
23.	Q0ECRP	Hypothetical protein A-105 -	110	4	4	2.92	0
24.	YP12_RTBVP	HYPOTHETICAL P12 PROTEIN (ORF	110	4	4	2.92	0
25.	YP12_RTBV	HYPOTHETICAL P12 PROTEIN (ORF	110	4	4	2.92	0
26.	B40785	*ORF2 protein - Rice tungro b	110	4	4	2.92	0
27.	S16667	*Hypothetical protein P12 - R	110	4	4	2.92	0
28.	P70092	Sequence encoded by (2'-5') o	111	4	4	2.92	0
29.	S18858	*Cytochrome c-553 - Anabaena	111	4	4	2.92	0
30.	S22481	*Cytochrome c553 precursor -	111	4	4	2.92	0
31.	P71705	Partial (2'-5') oligo A synth	112	4	4	2.92	0
32.	NO75_PEA	EARLY NODULIN-75 PROTEIN (N-7	112	4	4	2.92	0
33.	S10101	*Nodulation protein ENOD2 - G	114	4	4	2.92	0
34.	YCW8_YEAST	HYPOTHETICAL 12.4 KD PROTEIN	114	4	4	2.92	0
35.	S19492	Hypothetical protein YCR78C -	132	4	4	2.92	0
36.	R05445	CAT-A4-751i hybrid protein.	137	4	4	2.92	0
37.	CY2_RHOCA	CYTOCHROME C2 PRECURSOR.	137	4	4	2.92	0
38.	CCRF2C	Cytochrome c2 precursor - Rho	146	4	4	2.92	0
39.	YZP2_ECOLI	VERY HYPOTHETICAL 16.1 KD PRO	146	4	4	2.92	0
40.	A35720	*Hypothetical protein 146 (ph	160	4	4	2.92	0
41.	PETD_PROHO	CYTOCHROME B6-F COMPLEX SUBUN	160	4	4	2.92	0
42.	S16853	*petD protein chain IV - Proc	175	4	4	2.92	0
43.	MAT1_YEAST	MATING HORMONE ALPHA-1.	175	4	4	2.92	0
44.	COAG_LIMPO	COAGULOGEN (CONTAINS: COAGULI	175	4	4	2.92	0
45.	S19453	Mating hormone alpha-1 - Yeas	175	4	4	2.92	0
46.	S19397	Mating hormone alpha-1 - Yeas	175	4	4	2.92	0
47.	WCHCA	Coagulogen - Atlantic horsesh	175	4	4	2.92	0
48.	JFBYA1	Mating hormone alpha-1 - Yeas	179	4	4	2.92	0
49.	SPC4_CANFA	MICROSOMAL SIGNAL PEPTIDASE 1	179	4	4	2.92	0
50.	A35309	*Signal peptidase 18K chain -					

No alignments saved.

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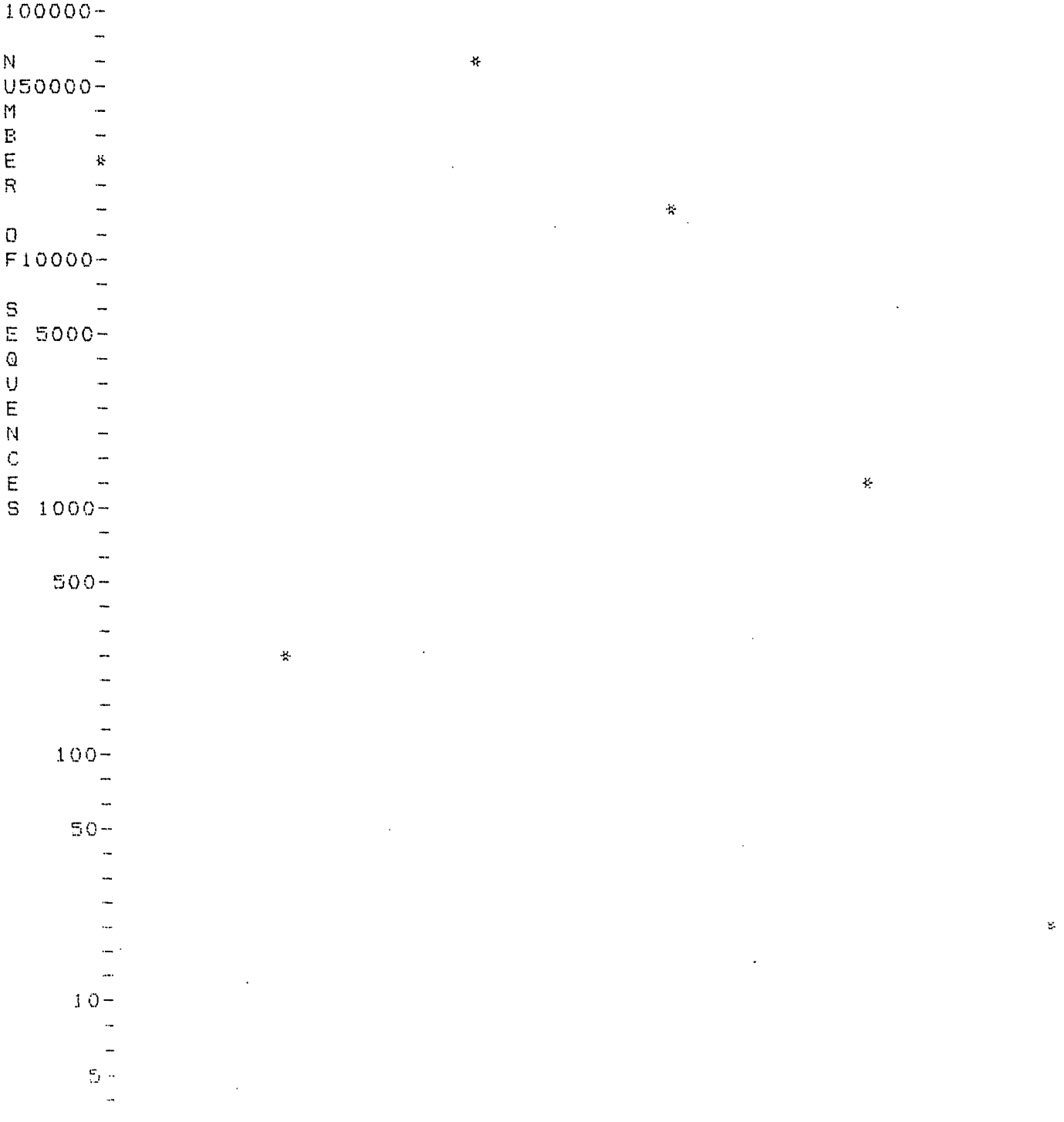
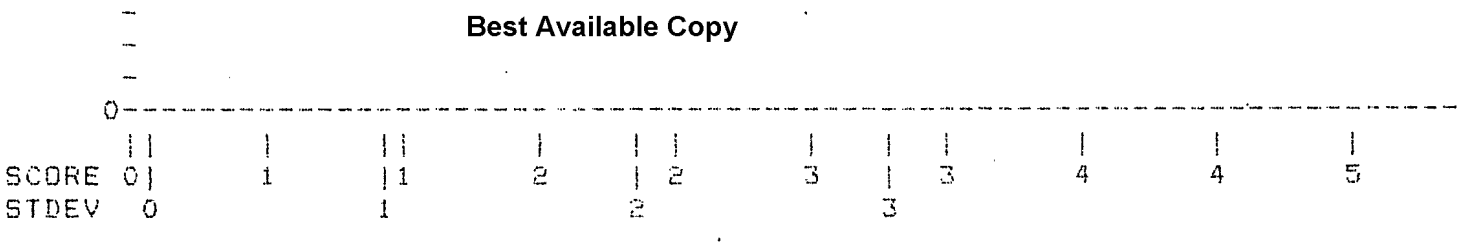
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-4.res made by alexk on Thu 25 Feb 93 10:41:56-PST.

Query sequence being compared: CELSA-4 (1-5)
Number of sequences searched: 94553
Number of scores above cutoff: 4622

Results of the initial comparison of CELSA-4 (1-5) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.04

Times:	CPU	Total Elapsed
	00:03:29.98	00:03:54.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4622

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

17 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. S20590	*Sialidase - Actinomyces visc	913	5	5	3.84	0
2. A33827	*Regulatory protein ral2 - Ye	611	5	5	3.84	0
3. RAL2_SCHPO	RAL2 PROTEIN.	611	5	5	3.84	0
4. WMCVFM	Inclusion body matrix protein	512	5	5	3.84	0
5. IBMP_FMVD	INCLUSION BODY MATRIX PROTEIN	512	5	5	3.84	0
6. A30828	Steroid 17alpha-monooxygenase	507	5	5	3.84	0
7. S16719	*Steroid 17alpha-monooxygenas	507	5	5	3.84	0
8. CPT1_RAT	CYTOCHROME P450 XVIIA1 (P450-	507	5	5	3.84	0
9. JH0594	Vasoactive intestinal polypep	459	5	5	3.84	0
10. S16562	*nolF protein - Rhizobium mel	367	5	5	3.84	0
11. NOLF_RHIME	NODULATION PROTEIN NOLF.	367	5	5	3.84	0
12. A27659	Cytochrome P450 17 - Rat (Fra	507	5	5	3.84	0
13. A33980	Steroid 17alpha-monooxygenase	235	5	5	3.84	0
14. S18659	*Hypothetical protein - Mycop	143	5	5	3.84	0
15. R20793	CDR-grafted, humanised heavy	146	5	5	3.84	0
16. S06727	*Hypothetical protein 1 (mini	122	5	5	3.84	0
17. YM2_STRCO	MINI-CIRCLE HYPOTHETICAL 12.3	121	5	5	3.84	0

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
18. A35776	*RecQ protein - Escherichia c	5	4	4	2.88	0
19. S04171	aadA protein - Klebsiella pne	23	4	4	2.88	0
20. RP30_YEAST	RIBOSOMAL PROTEIN RP30 (FRAGM	25	4	4	2.88	0
21. P90810	Synthetic HTLV-I peptide anti	26	4	4	2.88	0
22. D41161	*31K antigen PEB4 - Campyloba	34	4	4	2.88	0
23. R13186	Peptide VII immunoreactive wi	38	4	4	2.88	0
24. R06408	HTLV-1 corresponding peptide	38	4	4	2.88	0
25. S10765	*Glutamate synthase - Azospir	40	4	4	2.88	0
26. R20772	Peptide V based on immunoreac	40	4	4	2.88	0
27. R13185	Peptide (V) immunoreactive wi	40	4	4	2.88	0
28. R13591	HTLV-I env precursor epitope	40	4	4	2.88	0
29. TYBB_SALGA	THYMOSIN BETA-12.	42	4	4	2.88	0
30. LCA_MACGI	ALPHA-LACTALBUMIN I (LACTOSE	42	4	4	2.88	0
31. B39880	*Streptomycin/spectinomycin r	42	4	4	2.88	0
32. A10265	alpha-Lactalbumin I - Eastern	42	4	4	2.88	0
33. THIO_EUBAC	THIOREDOXIN (FRAGMENT).	45	4	4	2.88	0
34. PSBK_CHLRE	PHOTOSYSTEM II 4 KD REACTION	46	4	4	2.88	0
35. S11162	Photosystem II protein psbK p	46	4	4	2.88	0
36. PSBK_MARPO	PHOTOSYSTEM II 4 KD REACTION	55	4	4	2.88	0
37. S01585	Photosystem II protein psbK p	55	4	4	2.88	0
38. A05024	Hypothetical protein 55 - Liv	55	4	4	2.88	0
39. PSBK_TOBAC	PHOTOSYSTEM II 4 KD REACTION	61	4	4	2.88	0
40. PSBK_SINAL	PHOTOSYSTEM II 4 KD REACTION	61	4	4	2.88	0
41. PSBK_ORYSA	PHOTOSYSTEM II 4 KD REACTION	61	4	4	2.88	0
42. PSBK_HORVU	PHOTOSYSTEM II 4 KD REACTION	61	4	4	2.88	0
43. S02115	Photosystem II protein psbK p	61	4	4	2.88	0
44. F2RZK5	Photosystem II protein psbK -	61	4	4	2.88	0
45. E26839	Streptomycin/spectinomycin re	63	4	4	2.88	0
46. R13345	P1684 HCV antigen (1684-1750)	67	4	4	2.88	0
47. A41474	*Heat-stable enterotoxin yst	71	4	4	2.88	0
48. S11707	*Aminoglycoside adenylyltrans	72	4	4	2.88	0
49. R10026	ompA Signal peptide used to c	78	4	4	2.88	0
50. CPB3_ECOLI	COPB PROTEIN (REPA2 PROTEIN).	84	4	4	2.88	0

No alignments saved.

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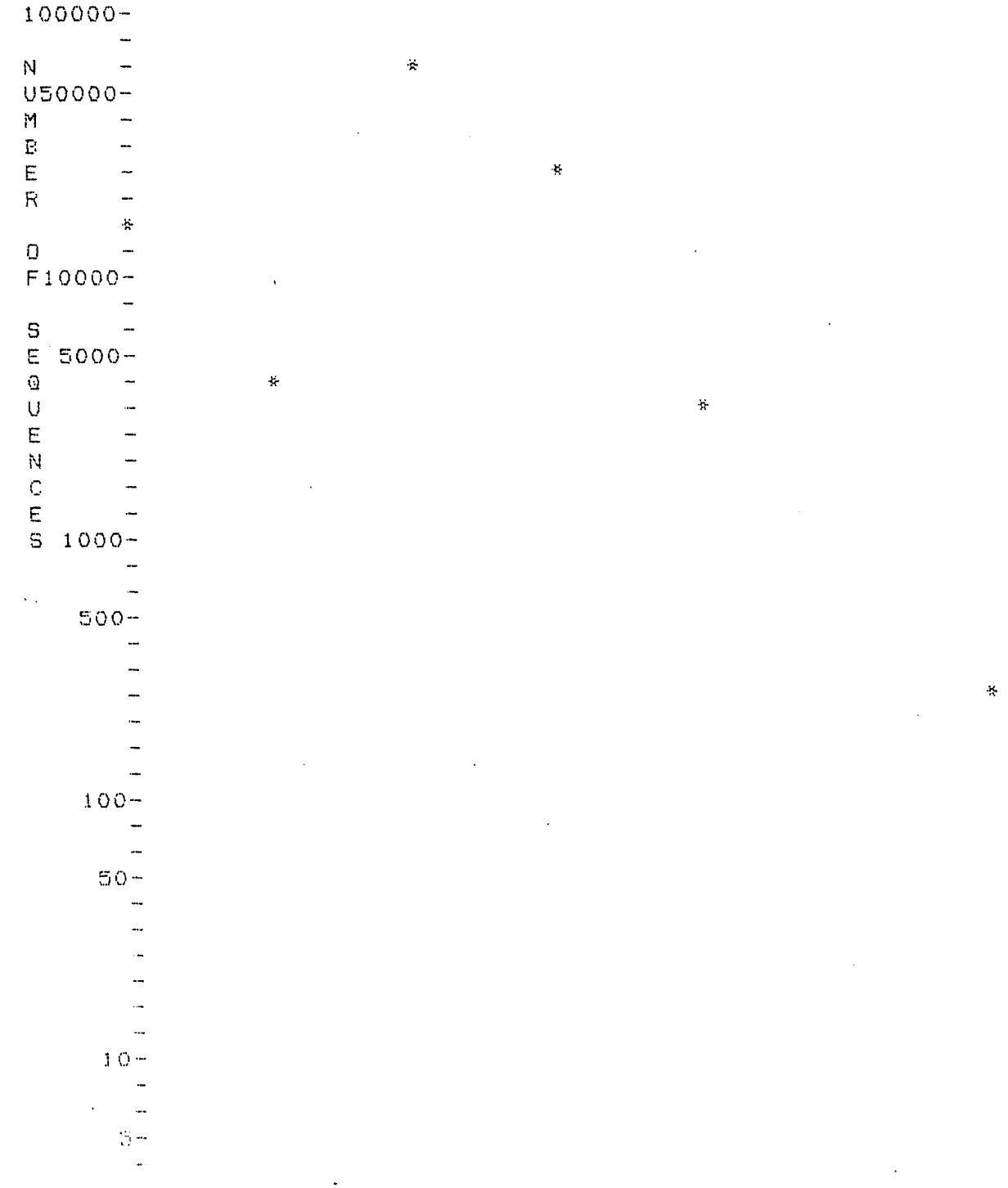
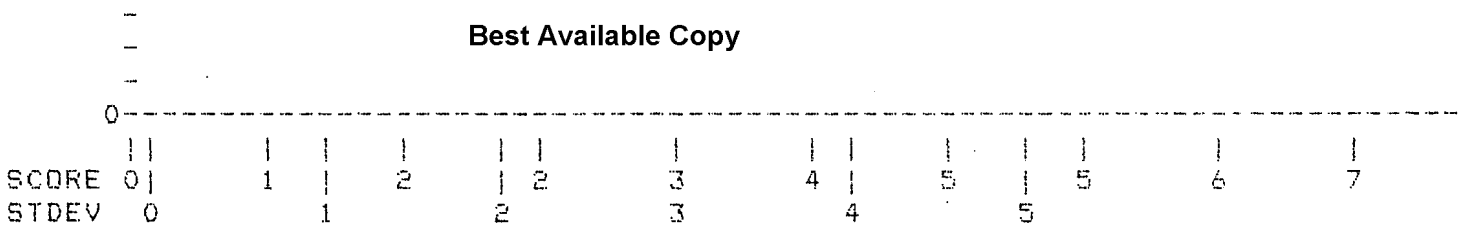
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-5.res made by alexk on Thu 25 Feb 93 10:21:15-PST.

Query sequence being compared: CELSA-5 (1-10)
Number of sequences searched: 94553
Number of scores above cutoff: 3851

Results of the initial comparison of CELSA-5 (1-10) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.01

Times:	CPU	Total Elapsed
	00:03:30.00	00:07:13.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 3851

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 5 standard deviations above mean ****					
1.	LACP_KLULA	LACTOSE PERMEASE.	587	7	7	5.92	0
2.	A31776	Lactose permease - Yeast (Klu	587	7	7	5.92	0
		**** 4 standard deviations above mean ****					
3.	S13898	*Alkaline phosphatase - Rabbi	16	6	6	4.93	0
4.	MCP5_MOUSE	MAST CELL PROTEASE 5 (EC 3.4.	30	6	7	4.93	0
5.	C35646	*Mast cell proteinase MMCP-5	30	6	7	4.93	0
6.	R15700	Human tumour-associated cell	30	6	6	4.93	0
7.	A29064	Proglucagon - Pig (fragment)	48	6	7	4.93	0
8.	P91880	Fusion protein coded for by o	50	6	7	4.93	0
9.	P92100	Fusion protein coded for by o	63	6	7	4.93	0
10.	VE6_BPV4	PROBABLE E6 PROTEIN.	99	6	6	4.93	0
11.	WoWI84	E6 protein - Bovine papilloma	99	6	6	4.93	0
12.	B40093	*Ubiquitin carboxyl-terminal	102	6	7	4.93	0
13.	CYC_CAINT	CYTOCHROME C	111	6	6	4.93	0

16.	CYC_NIGDA	CYTOCHROME C.	111	6	6	4.93	0
17.	CYC_MAIZE	CYTOCHROME C.	111	6	6	4.93	0
18.	CYC_HELAN	CYTOCHROME C.	111	6	6	4.93	0
19.	CYC_CUCMA	CYTOCHROME C.	111	6	6	4.93	0
20.	CYC_BRAOL	CYTOCHROME C.	111	6	6	4.93	0
21.	CYC_ARUMA	CYTOCHROME C.	111	6	6	4.93	0
22.	CCFS	Cytochrome c - Common sunflow	111	6	6	4.93	0
23.	CCND	Cytochrome c - Love-in-a-mist	111	6	6	4.93	0
24.	CCRM	Cytochrome c - Cuckoopint	111	6	6	4.93	0
25.	CCED	Cytochrome c - European elder	111	6	6	4.93	0
26.	CCZM	Cytochrome c - Maize	111	6	6	4.93	0
27.	CCRZ	Cytochrome c - Rice	111	6	6	4.93	0
28.	CCMB	Cytochrome c - Mung bean	111	6	6	4.93	0
29.	CCFU	Cytochrome c - Cucurbit	111	6	6	4.93	0
30.	CCRPBO	Cytochrome c - Cauliflower	111	6	6	4.93	0
31.	CCRPBN	Cytochrome c - Rape	111	6	6	4.93	0
32.	CYC_WHEAT	CYTOCHROME C.	112	6	6	4.93	0
33.	JS0709	Cytochrome c - Rice	112	6	6	4.93	0
34.	CCWT	Cytochrome c - Wheat	112	6	6	4.93	0
35.	S21626	*Collagen alpha 1(I) chain -	147	6	6	4.93	0
36.	P70557	Tumor necrosis factor.	154	6	6	4.93	0
37.	P60526	Sequence of tumour necrosis f	156	6	6	4.93	0
38.	P60527	Sequence of tumour necrosis f	157	6	6	4.93	0
39.	GLUC_PIG	GLUCAGON PRECURSOR (FRAGMENT)	158	6	7	4.93	0
40.	P70558	Tumor necrosis factor.	170	6	6	4.93	0
41.	YCED_ECOL1	HYPOTHETICAL 19.3 KD PROTEIN	173	6	6	4.93	0
42.	JV0047	Hypothetical 30K protein (rpm	173	6	6	4.93	0
43.	GLUC_OCTDE	GLUCAGON PRECURSOR.	180	6	7	4.93	0
44.	GLUC_MESAU	GLUCAGON PRECURSOR.	180	6	7	4.93	0
45.	C36118	*Proglucagon precursor - Degu	180	6	7	4.93	0
46.	GCHY	Proglucagon precursor - Golde	180	6	7	4.93	0
47.	R04190	Peptide derived from gp120 en	180	6	6	4.93	0
48.	TRIF_CHICK	TROPONIN I, FAST SKELETAL MUS	182	6	6	4.93	0
49.	TPCHIS	Troponin I, fast skeletal mus	182	6	6	4.93	0
50.	A24918	Troponin I, fast skeletal mus	183	6	6	4.93	0

No alignments saved.

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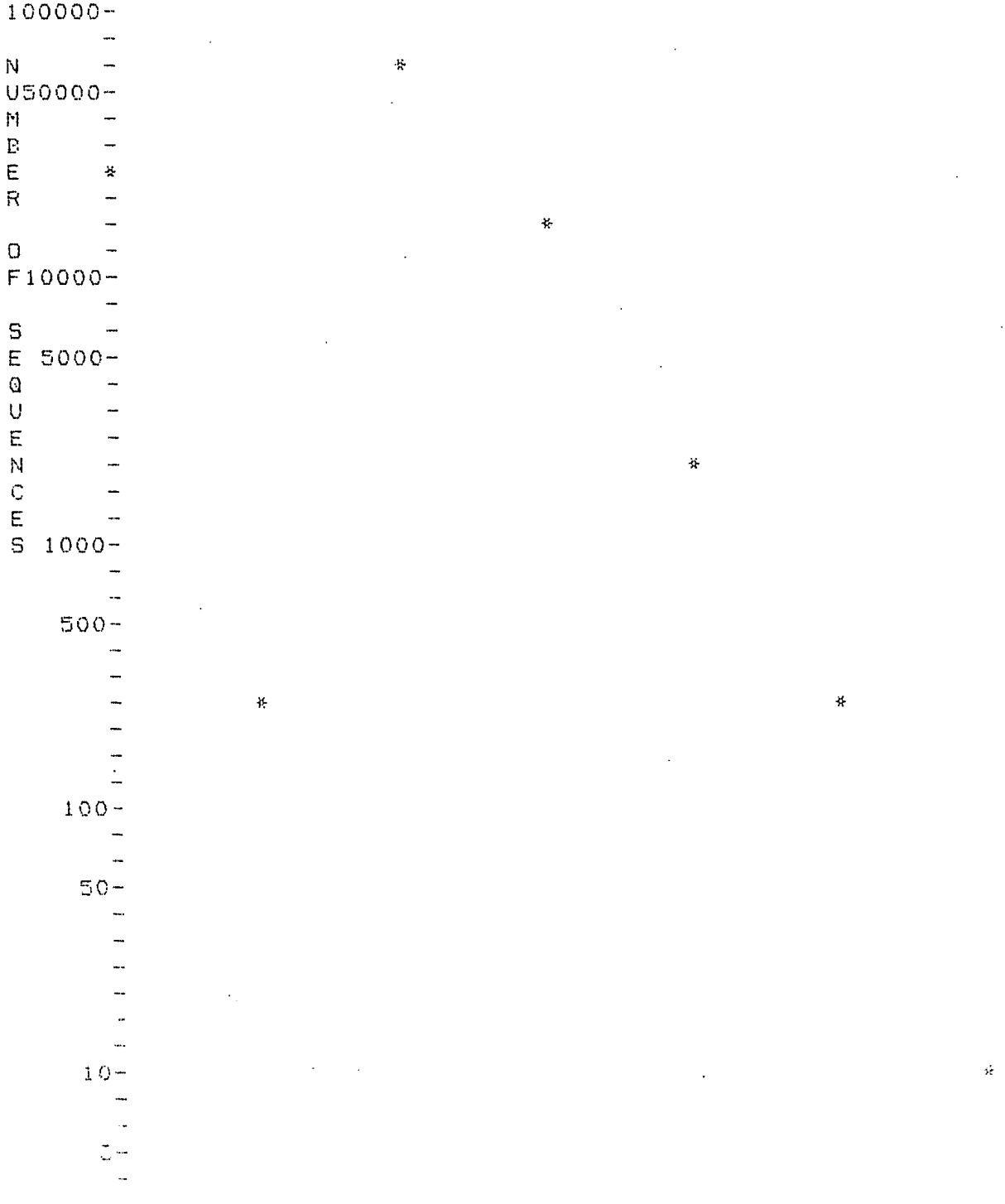
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-6.res made by alexk on Thu 25 Feb 93 10:28:59-PST.

Query sequence being compared: CELSA-6 (1-9)
Number of sequences searched: 94553
Number of scores above cutoff: 3802

Results of the initial comparison of CELSA-6 (1-9) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries



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 0 -------------------------------------------------------------------------------
   ||     |    |     |      | |        |        | |      |     |  |       |       |
SCORE 0|     1    |     2     | 2        3        4 |      5     |  5       6       7
STDEV  0          1           2          3          4           5
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	1	3	1.05

	CPU	Total Elapsed
Times:	00:03:24.97	00:06:53.00

Number of residues:	25433612
Number of sequences searched:	94553
Number of scores above cutoff:	3802

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 5 standard deviations above mean ****					
1. VG01_BPP22	PORTAL PROTEIN (PROTEIN GP1).	724	7	7	5.70	0
2. Z1BP22	Gene 1 protein - Phage P22	725	7	7	5.70	0
	**** 4 standard deviations above mean ****					
3. RECO_BOVIN	RECOVERIN (P26).	202	6	6	4.75	0
4. S21155	*23K protein - Mouse	202	6	6	4.75	0
5. A38433	*Recoverin - Bovine	202	6	6	4.75	0
6. S19305	*Calcium binding protein P26	202	6	6	4.75	0
7. ATC2_YEAST	PROBABLE CALCIUM-TRANSPORTING	1091	6	6	4.75	0
8. PWBYR2	Ca2+-transporting ATPase PMR2	1091	6	6	4.75	0
9. CYGS_STRPU	SPERACT RECEPTOR PRECURSOR (G	1125	6	6	4.75	0
10. A33535	*Guanylate cyclase precursor	1125	6	6	4.75	0
11. A30856	*Guanylate cyclase - Sea urch	1125	6	6	4.75	0
	**** 3 standard deviations above mean ****					
12. [illegible]	[illegible] (FRAGMENT)	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
13. [illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

15.	VKIL_BPP22	KIL PROTEIN.	62	5	5	3.80	0
16.	VDBP22	kil protein - Phage P22	62	5	5	3.80	0
17.	FER1_EQUTE	FERREDOXIN I.	95	5	5	3.80	0
18.	FER1_EQUAR	FERREDOXIN I.	95	5	5	3.80	0
19.	FEEQ1F	Ferredoxin I - Field horsetai	95	5	5	3.80	0
20.	FEEQ1	Ferredoxin I - Horsetail (Equ	95	5	5	3.80	0
21.	CYTC_BOVIN	CYSTATIN, COLOSTRUM (THIOL PR	112	5	6	3.80	0
22.	UDBO	Cystatin - Bovine	112	5	6	3.80	0
23.	P30180	Sequence of a polypeptide wit	155	5	5	3.80	0
24.	P40124	Sequence encoded by the cDNA	155	5	5	3.80	0
25.	LEPA_PSEFL	LEPA PROTEIN (FRAGMENT).	161	5	5	3.80	0
26.	P60691	Sequence of the region coding	161	5	5	3.80	0
27.	P80055	Sequence of human interferon	161	5	5	3.80	0
28.	P50281	Protein sequence encoding mod	164	5	5	3.80	0
29.	P30227	Sequence of hybrid interferon	165	5	5	3.80	0
30.	P50207	Modified human interferon (IF	165	5	5	3.80	0
31.	P50280	Protein sequence encoding mod	165	5	5	3.80	0
32.	P50273	Protein sequence encoding mod	165	5	5	3.80	0
33.	S04479	*Interferon beta-1 - Human	166	5	5	3.80	0
34.	P30222	Sequence of hybrid interferon	166	5	5	3.80	0
35.	P30219	Sequence of interferon (HuIFN	166	5	5	3.80	0
36.	P40626	Sequence of interferon-beta-S	166	5	5	3.80	0
37.	P50206	Modified human interferon (IF	166	5	5	3.80	0
38.	P50197	Modified human interferon (IF	166	5	5	3.80	0
39.	P50196	Modified human interferon (IF	166	5	5	3.80	0
40.	P50195	Modified human interferon (IF	166	5	5	3.80	0
41.	P50194	Modified human interferon (IF	166	5	5	3.80	0
42.	P50193	Modified human interferon (IF	166	5	5	3.80	0
43.	P50192	Modified human interferon (IF	166	5	5	3.80	0
44.	P50279	Protein sequence encoding syn	166	5	5	3.80	0
45.	P50278	Protein sequence encoding mod	166	5	5	3.80	0
46.	P50277	Protein sequence encoding mod	166	5	5	3.80	0
47.	P50276	Protein sequence encoding mod	166	5	5	3.80	0
48.	P50275	Protein sequence encoding mod	166	5	5	3.80	0
49.	P50274	Protein sequence encoding mod	166	5	5	3.80	0
50.	P50272	Protein sequence encoding mod	166	5	5	3.80	0

No alignments saved.

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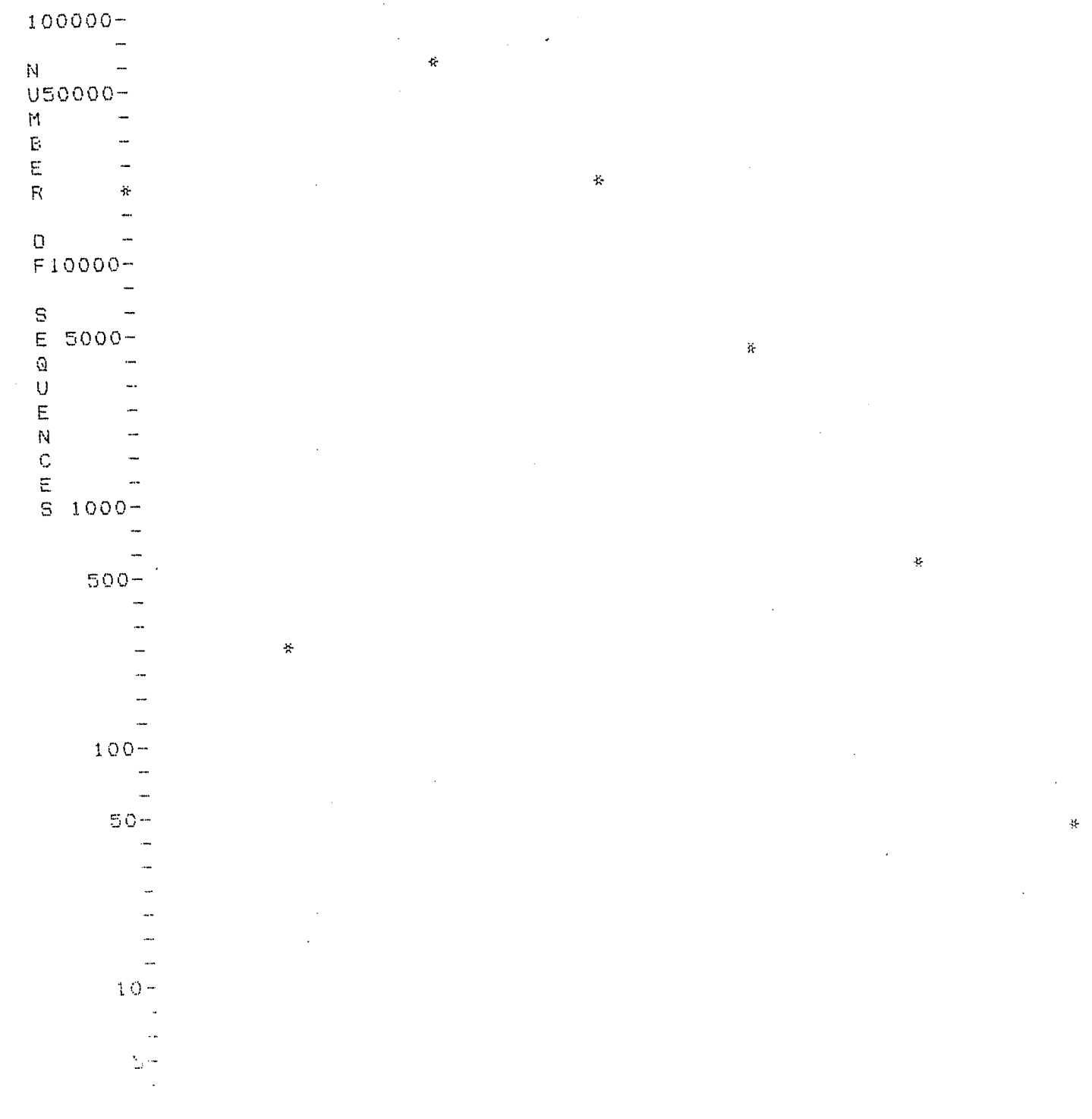
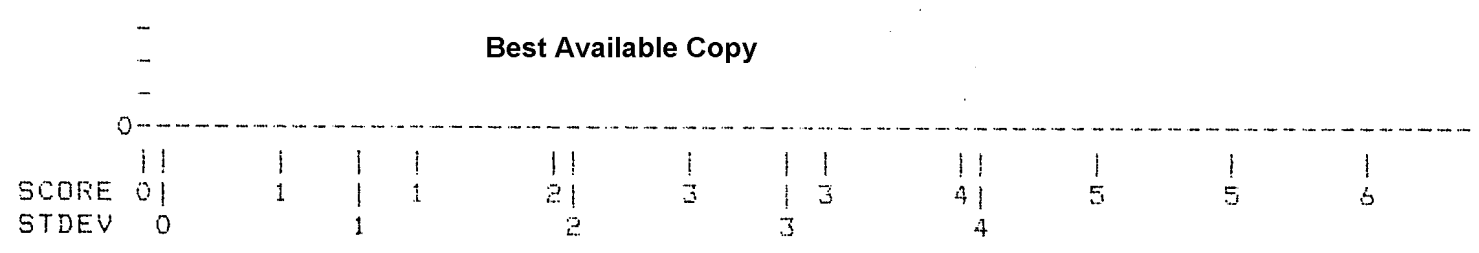
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-7.res made by alexk on Thu 25 Feb 93 10:37:07-PST.

Query sequence being compared: CELSA-7 (1-10)
Number of sequences searched: 94553
Number of scores above cutoff: 3985

Results of the initial comparison of CELSA-7 (1-10) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.07

Times:	CPU	Total Elapsed
	00:03:25.11	00:07:03.00

Number of residues:	25433612
Number of sequences searched:	94553
Number of scores above cutoff:	3985

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 4 standard deviations above mean ****					
1.	YCA8_YEAST	HYPOTHETICAL 13.1 KD PROTEIN	119	6	6	4.69	0
2.	S19410	Hypothetical protein YCL8C -	119	6	6	4.69	0
3.	S17923	rbcL intron protein - Green a	274	6	6	4.69	0
4.	MTD1_DESDN	MODIFICATION METHYLASE DDEI (	413	6	7	4.69	0
5.	S00543	Site-specific methyltransfera	413	6	7	4.69	0
6.	AMYP_RAT	ALPHA-AMYLASE PANCREATIC PREC	503	6	6	4.69	0
7.	ALRTP	alpha-Amylase precursor, panc	503	6	6	4.69	0
8.	P50263	Sequence encoded by pancreati	507	6	6	4.69	0
9.	ALMSPC	alpha-Amylase 3(C) precursor,	508	6	6	4.69	0
10.	ALMSP1	alpha-Amylase A1 precursor - p	508	6	6	4.69	0
11.	AMYS_MOUSE	ALPHA-AMYLASE SALIVARY AND PE	511	6	6	4.69	0
12.	ALMSS	alpha-Amylase precursor, sali	511	6	6	4.69	0
13.	AVR1_MOUSE	ACTIVIN RECEPTOR TYPE I PRECU	513	6	6	4.69	0
14.	AVR1_HUMAN	ACTIVIN RECEPTOR TYPE I PRECU	513	6	6	4.69	0
15.	S37914						

17.	S22345	*Activin receptor - Human	513	6	6	4.69	0
18.	J01486	Activin receptor II precursor	513	6	6	4.69	0
19.	A37913	*mik1 protein - Yeast (Schizo	581	6	6	4.69	0
20.	SWI5_YEAST	TRANSCRIPTIONAL FACTOR SWI5.	709	6	6	4.69	0
21.	TWBYS5	Transcription factor SWI5 - Y	709	6	6	4.69	0
22.	S18512	Cell division control protein	1035	6	6	4.69	0
23.	POLG_POL1M	GENOME POLYPROTEIN (COAT PROT	2207	6	6	4.69	0
24.	S09553	Genome polyprotein - Human po	2207	6	6	4.69	0
25.	GNNY1P	Genome polyprotein (version 1	2207	6	6	4.69	0
26.	POLH_POL1M	GENOME POLYPROTEIN (COAT PROT	2209	6	6	4.69	0
27.	POLG_POL1S	GENOME POLYPROTEIN (COAT PROT	2209	6	6	4.69	0
28.	GNNY3P	Genome polyprotein - Human po	2209	6	6	4.69	0
29.	GNNY2P	Genome polyprotein (version 2	2209	6	6	4.69	0
30.	A37113	*Ryanodine receptor, cardiac	4969	6	6	4.69	0
31.	R10834	Rianodin receptor.	4987	6	6	4.69	0
32.	RYNR_HUMAN	RYANODINE RECEPTOR, SKELETAL	5032	6	6	4.69	0
33.	A35041	*Ryanodine receptor - Human	5032	6	6	4.69	0
34.	B35041	*Ryanodine receptor - Rabbit	5034	6	6	4.69	0
35.	S18135	*Calcium release channel - Pi	5034	6	6	4.69	0
36.	RYNR_RABIT	RYANODINE RECEPTOR, SKELETAL	5037	6	6	4.69	0
37.	S04654	Ryanodine receptor - Rabbit	5037	6	6	4.69	0
38.	R11510	Ryanodine receptor deduced fr	5072	6	6	4.69	0
		**** 3 standard deviations above mean ****					
39.	R04972	Papilloma virus type 16 L1 pe	20	5	5	3.75	0
40.	P81545	Human insulin acceptor protei	33	5	5	3.75	0
41.	A36357	*Cytochrome-c oxidase chain I	66	5	5	3.75	0
42.	NXL3_DENPO	LONG NEUROTOXIN 3 (TOXIN VN2)	72	5	5	3.75	0
43.	NXL2_DENPO	LONG NEUROTOXIN 2 (NEUROTOXIN	72	5	5	3.75	0
44.	NXL1_DENPO	LONG NEUROTOXIN 1 (NEUROTOXIN	72	5	5	3.75	0
45.	N2EP2D	Long neurotoxin 2 - Black mam	72	5	5	3.75	0
46.	N2EP1D	Long neurotoxin 1 - Black mam	72	5	5	3.75	0
47.	A35991	*Retinoic acid receptor gamma	74	5	5	3.75	0
48.	THIO_BPT4	THIOREDOXIN.	87	5	5	3.75	0
49.	G30292	*Gene nrdC protein - Phage T4	87	5	5	3.75	0
50.	TXBPT4	Thioredoxin - Phage T4	87	5	5	3.75	0

No alignments saved.

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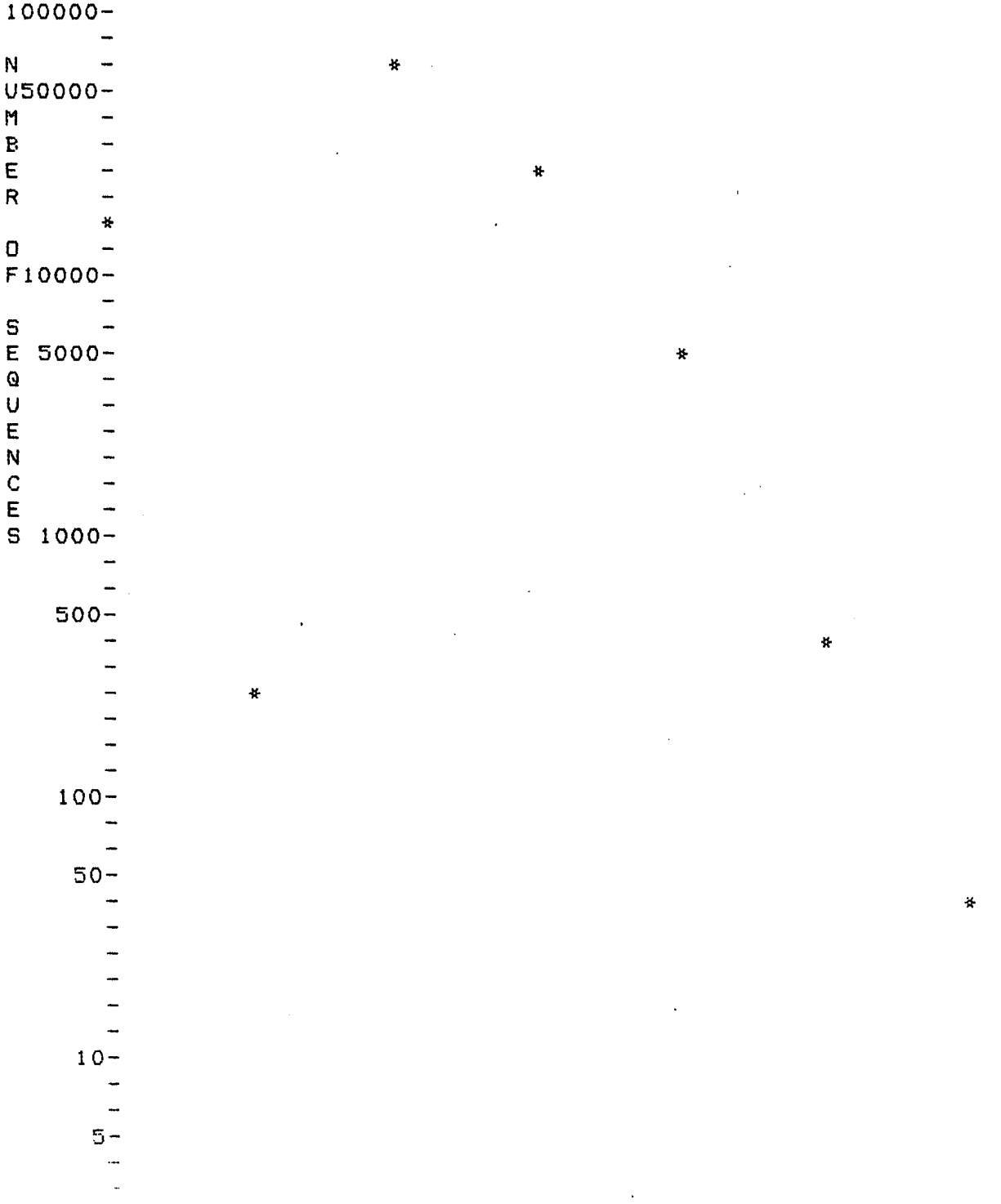
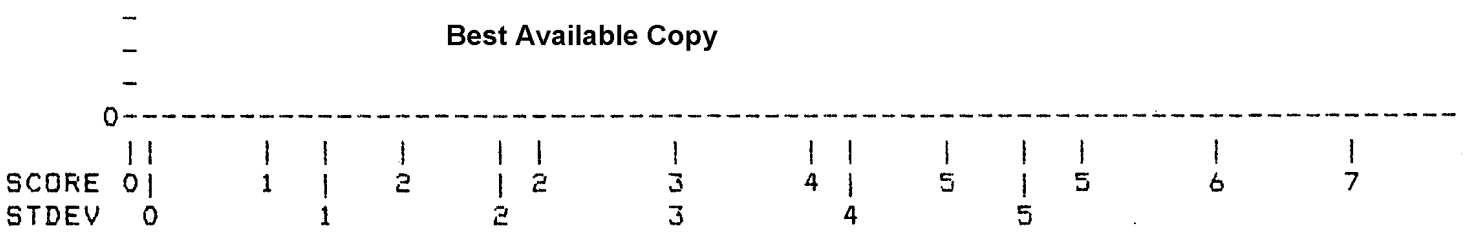
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-8.res made by alexk on Thu 25 Feb 93 10:24:25-PST.

Query sequence being compared: CELSA-8 (1-11)
Number of sequences searched: 94553
Number of scores above cutoff: 3979

Results of the initial comparison of CELSA-8 (1-11) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.04

Times:	CPU	Total Elapsed
	00:03:41.11	00:08:23.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 3979

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 5 standard deviations above mean ****					
1. FAS_CHICK	FATTY ACID SYNTHASE (EC 2.3.1	2446	7	7	5.77	0
2. XYCHFA	Fatty-acid synthase - Chicken	2446	7	7	5.77	0
	**** 4 standard deviations above mean ****					
3. P70030	Secretory signal sequence of	26	6	6	4.81	0
4. P70033	Secretory signal sequence of	39	6	6	4.81	0
5. P70029	Secretory signal sequence of	50	6	6	4.81	0
6. S17024	Hypothetical protein (IFM1 3'	124	6	6	4.81	0
7. YIFM_YEAST	HYPOTHETICAL PROTEIN IN IFM1	125	6	6	4.81	0
8. S20178	*Hypothetical protein - Yeast	125	6	6	4.81	0
9. FMC1_ECOLI	CFA/I FIMBRIAL SUBUNIT B PREC	170	6	6	4.81	0
10. YQECC1	CFA1 fimbrial protein precurs	170	6	6	4.81	0
11. SSBR_ECOLI	SINGLE-STRAND BINDING PROTEIN	174	6	6	4.81	0
12. SSBP_ECOLI	SINGLE-STRAND BINDING PROTEIN	174	6	6	4.81	0
13. A38487	*Helix-destabilizing protein	174	6	6	4.81	0
14. DDECIB	Helix-destabilizing protein -	175	6	6	4.81	0

16.	IBP3_HUMAN	INSULIN-LIKE GROWTH FACTOR BI	291	6	6	4.81	0
17.	A34651	*Insulin-like growth factor b	291	6	6	4.81	0
18.	IOHU3	Insulin-like growth factor bi	291	6	6	4.81	0
19.	R05596	Somatomedin carrier protein s	291	6	6	4.81	0
20.	P92300	Sequence of human insulin-lik	291	6	6	4.81	0
21.	IBP3_RAT	INSULIN-LIKE GROWTH FACTOR BI	292	6	6	4.81	0
22.	A36748	*Insulin-like growth factor b	292	6	6	4.81	0
23.	S11738	Hemagglutinin precursor - Inf	378	6	7	4.81	0
24.	A39314	*Gastricsin precursor - Bullf	384	6	6	4.81	0
25.	PEPC_HUMAN	PROGASTRICSIN PRECURSOR (EC 3	388	6	6	4.81	0
26.	A29937	*Gastricsin precursor - Human	388	6	6	4.81	0
27.	A31811	*Gastricsin precursor - Human	388	6	6	4.81	0
28.	PEPC_RAT	GASTRICSIN PRECURSOR (EC 3.4.	392	6	6	4.81	0
29.	A33510	*Gastricsin - Rat #EC-number	392	6	6	4.81	0
30.	A24608	Pepsin A precursor - Rat #EC-	392	6	6	4.81	0
31.	YAJA_ECOLI	HYPOTHETICAL 44.7 KD PROTEIN	400	6	7	4.81	0
32.	JS0349	Hypothetical 45K protein (sbc	400	6	7	4.81	0
33.	CYAA_TRYEQ	ADENYLATE CYCLASE (EC 4.6.1.1	469	6	6	4.81	0
34.	S16359	Adenylate cyclase - Trypanoso	469	6	6	4.81	0
35.	OM6E_CHLTR	60 KD OUTER MEMBRANE PROTEIN	547	6	6	4.81	0
36.	S13120	*Omp2 protein - Chlamydia tra	547	6	6	4.81	0
37.	PC1_MOUSE	PLASMA-CELL MEMBRANE GLYCOPRO	871	6	6	4.81	0
38.	A27410	Plasma cell membrane protein	905	6	6	4.81	0
39.	CARB_BACSU	CARBAMOYL-PHOSPHATE SYNTHASE	1071	6	6	4.81	0
40.	F39845	*Carbamyl phosphate synthase	1071	6	6	4.81	0
		**** 3 standard deviations above mean ****					
41.	P98464	Sequence of C. trachomatis se	14	5	5	3.85	0
42.	P98452	Sequence of C. trachomatis se	14	5	5	3.85	0
43.	P98448	Sequence of C. trachomatis se	14	5	5	3.85	0
44.	P98444	Sequence of C. trachomatis se	14	5	5	3.85	0
45.	P98468	Sequence of C. trachomatis se	14	5	5	3.85	0
46.	P98460	Sequence of C. trachomatis se	14	5	5	3.85	0
47.	YPS1_PLEBO	HYPOTHETICAL 4.6 KD PROTEIN (	40	5	5	3.85	0
48.	PSBJ_CYAPA	PHOTOSYSTEM II REACTION CENTR	40	5	6	3.85	0
49.	S08038	Hypothetical protein 1 - Plec	40	5	5	3.85	0
50.	PQ0104	Microbial serine proteinase I	41	5	5	3.85	0

No alignments saved.

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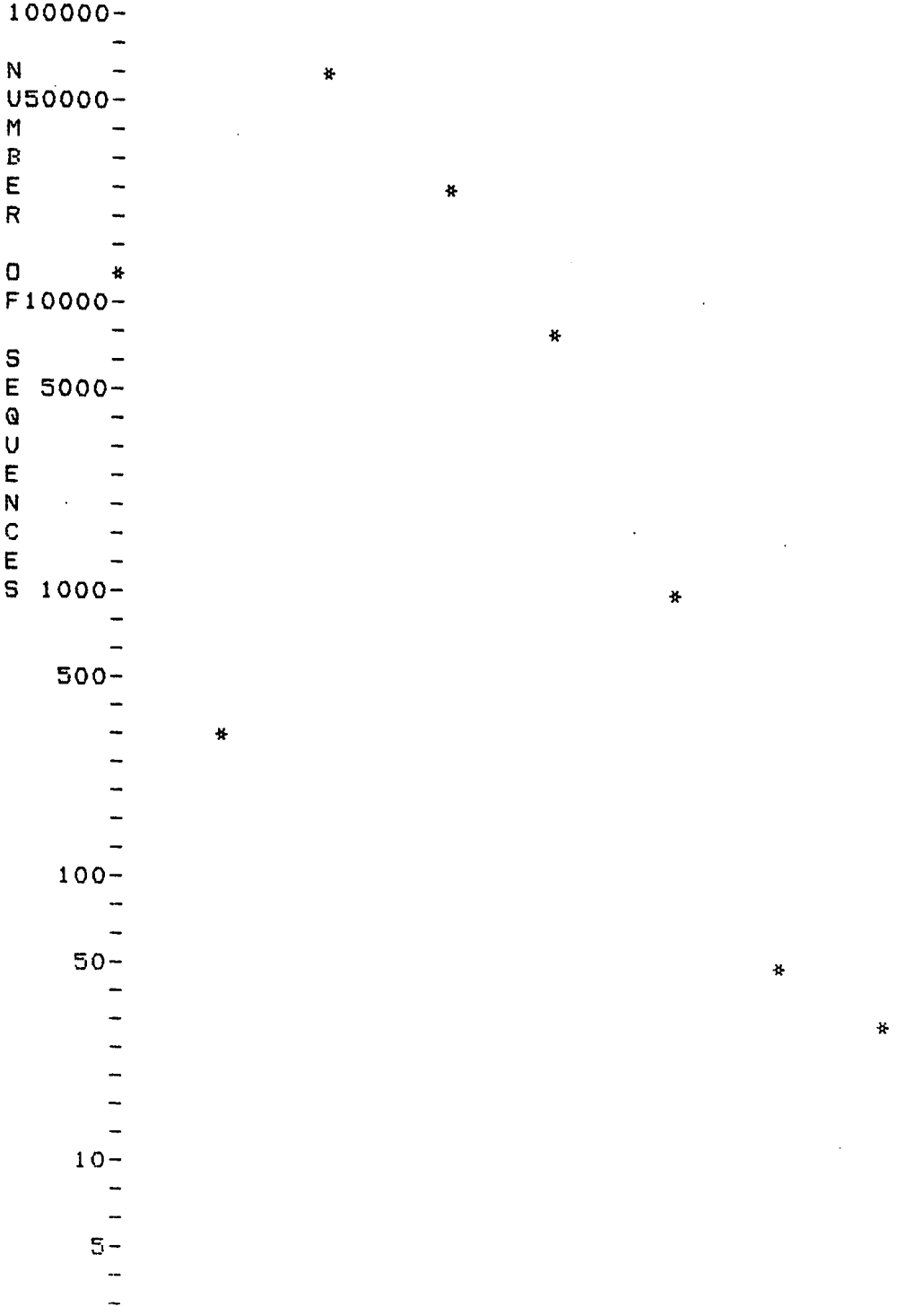
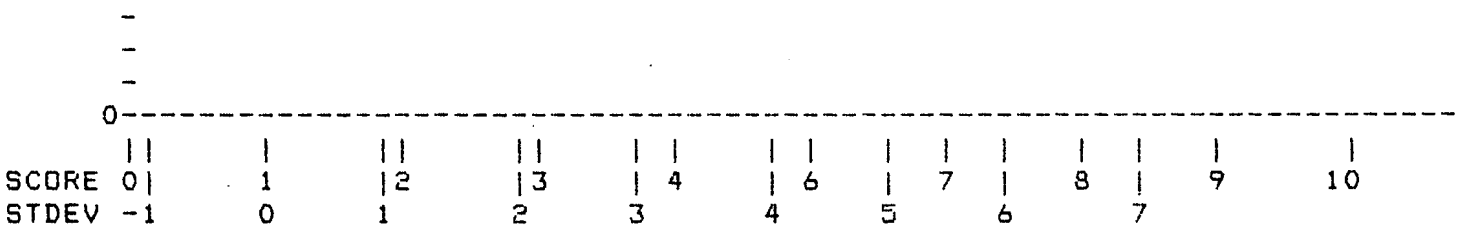
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-9.res made by alexk on Thu 25 Feb 93 10:39:58-PST.

Query sequence being compared: CELSA-9 (1-16)
Number of sequences searched: 94553
Number of scores above cutoff: 4422

Results of the initial comparison of CELSA-9 (1-16) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	3	1.06

Times:	CPU	Total Elapsed
	00:03:26.02	00:06:54.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4422

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 7 standard deviations above mean ****					
1. PC1_HUMAN	PLASMA-CELL MEMBRANE GLYCOPRO	873	10	11	7.58	0
2. S21706	*Pyrophosphatase - Human	925	10	11	7.58	0
3. A39216	*Plasma cell membrane protein	925	10	11	7.58	0
	**** 4 standard deviations above mean ****					
4. VD04_FOWP1	25.6 KD PROTEIN.	218	7	8	4.74	0
5. A35216	*FPD4 protein - Fowlpox virus	218	7	8	4.74	0
6. R21437	PE-40 protein contg. a methio	361	7	7	4.74	0
7. R21436	PE-40 somatostatin substitute	361	7	7	4.74	0
8. R21435	PE-40 somatostatin substitute	361	7	7	4.74	0
9. R20201	TGF-alpha-PE40ab.	419	7	7	4.74	0
10. R20199	TGF-alpha-PE40aB.	419	7	7	4.74	0
11. R07054	PE40AB protein comprising a p	419	7	7	4.74	0
12. R20200	TGF-alpha-PE40Ab.	420	7	7	4.74	0
13. R06450	TGF-alpha-PE40-ab modified ps	420	7	7	4.74	0
14. R06449	TGF-alpha-PE40-Ab modified ps	420	7	7	4.74	0

16.	R06447	TGF-57-Pseudomonas exotoxin 4	420	7	7	4.74	0
17.	R06994	PE40ab protein comprising a p	420	7	7	4.74	0
18.	R06992	PE40aB protein comprising a p	420	7	7	4.74	0
19.	R06993	PE40Ab protein comprising a p	420	7	7	4.74	0
20.	AMPL_BOVIN	LEUCINE AMINOPEPTIDASE (EC 3.	478	7	7	4.74	0
21.	APBOL	Cytosol aminopeptidase - Bovi	478	7	7	4.74	0
22.	R04934	Immunotoxin hybrid of human i	496	7	7	4.74	0
23.	R04920	Immunoprotein PEX46.	549	7	7	4.74	0
24.	R04923	Immunoprotein TANG11.	557	7	7	4.74	0
25.	R04919	Immunoprotein PEX45.	574	7	7	4.74	0
26.	R04924	Immunoprotein TANG12.	577	7	7	4.74	0
27.	TOXA_PSEAE	EXOTOXIN A PRECURSOR (NAD-DEP	638	7	7	4.74	0
28.	A30347	*Exotoxin A precursor - Pseud	638	7	7	4.74	0
29.	FEPA_ECOLI	FERRIC ENTEROCHELIN RECEPTOR	745	7	7	4.74	0
30.	QRECFC	Ferrienterochelin receptor pr	745	7	7	4.74	0
		**** 3 standard deviations above mean ****					
31.	PN0088	*Matrix protein M3 - Avian in	68	6	7	3.79	0
32.	PN0085	*Matrix protein M3 - Avian in	68	6	7	3.79	0
33.	ISS_ECOLI	HYPOTHETICAL ISS PROTEIN.	102	6	6	3.79	0
34.	JE0036	Hypothetical iss protein - Es	102	6	6	3.79	0
35.	ALB2_PEA	ALBUMIN 2 (PA2).	231	6	6	3.79	0
36.	S06248	Albumin 2 - Garden pea	231	6	6	3.79	0
37.	JQ0319	Hypothetical 27K protein - Xa	261	6	6	3.79	0
38.	ETB_STAAU	EXFOLIATIVE TOXIN B PRECURSOR	277	6	7	3.79	0
39.	PRSAEB	Epidermolytic toxin B precurs	277	6	7	3.79	0
40.	MIM1_CHICK	MYELOID PROTEIN-1 PRECURSOR.	326	6	6	3.79	0
41.	A33755	*myb-induced myeloid protein	326	6	6	3.79	0
42.	BYR1_SCHPO	PROTEIN KINASE BYR1 (EC 2.7.1	340	6	6	3.79	0
43.	OKBYR1	Protein kinase byr1 - Yeast (	340	6	6	3.79	0
44.	YPIX_CLOPE	HYPOTHETICAL 38.4 KD PROTEIN	342	6	7	3.79	0
45.	JT0370	Hypothetical protein g10 - Cl	342	6	7	3.79	0
46.	VMAT_SYNV	MATRIX PROTEIN (M2 PROTEIN).	345	6	7	3.79	0
47.	MFVNSY	Matrix protein - Sonchus yell	345	6	7	3.79	0
48.	K1CR_MOUSE	KERATIN, TYPE I CYTOSKELETAL	422	6	7	3.79	0
49.	JT0406	Keratin, type 1 cytoskeletal	423	6	7	3.79	0
50.	A25621	Endo B cytokeratin - Mouse	423	6	7	3.79	0

No alignments saved.

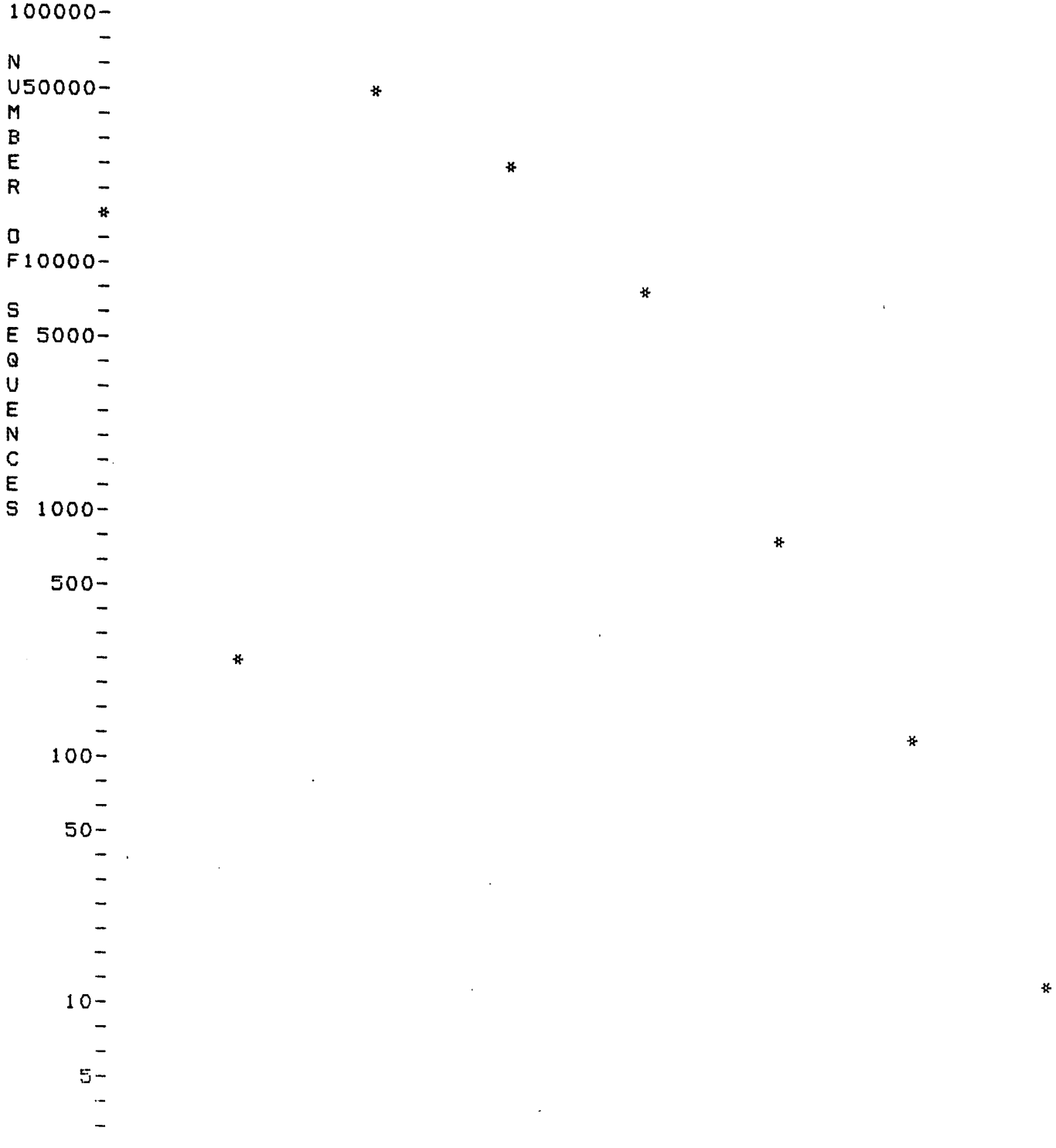
IntelliGenetics

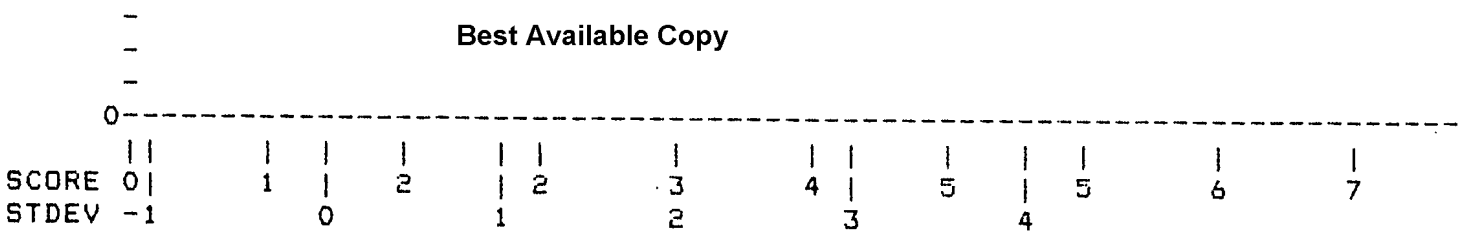
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celasa-10.res made by alexk on Thu 25 Feb 93 10:32:32-PST.

Query sequence being compared: CELASA-10 (1-12)
Number of sequences searched: 94553
Number of scores above cutoff: 4430

Results of the initial comparison of CELASA-10 (1-12) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	3	1.10

Times:	CPU	Total Elapsed
	00:03:25.96	00:07:28.00

Number of residues:	25433612
Number of sequences searched:	94553
Number of scores above cutoff:	4430

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 4 standard deviations above mean ****					
1. WMBEA1	Ribonucleoside-diphosphate re	321	7	7	4.56	0
2. A36062	*Catalase - Maize #EC-number	491	7	8	4.56	0
3. S18819	*Catalase - Maize #EC-number	491	7	8	4.56	0
4. CATA_IPOBA	CATALASE (EC 1.11.1.6).	492	7	8	4.56	0
5. CAT1_GOSHI	CATALASE ISOZYME A (EC 1.11.1	492	7	8	4.56	0
6. S07124	*Catalase - Sweet potato #EC-	492	7	8	4.56	0
7. S20999	*Catalase - Soybean #EC-numbe	492	7	8	4.56	0
8. S10770	*Catalase - Upland cotton #EC	492	7	8	4.56	0
9. S10395	Catalase chain 1 - Upland cot	492	7	8	4.56	0
10. CATA_PEA	CATALASE (EC 1.11.1.6).	494	7	8	4.56	0
11. S18346	Catalase - Garden pea #EC-num	494	7	8	4.56	0
	**** 3 standard deviations above mean ****					
12. C20554	Hemocyanin LpIIa - Atlantic h	20	6	6	3.65	0
13. A20554	Hemocyanin LpI chain - Atlant	24	6	6	3.65	0
14. F20554	Hemocyanin LpIV - Atlantic he	24	6	6	3.65	0

16.	S21559	*DNA gyrase chain B - Lyme di	84	6	6	3.65	0
17.	A28002	Apolipoprotein B-48 - Human (	106	6	6	3.65	0
18.	JN0145	Hypothetical 13.6K protein (d	117	6	7	3.65	0
19.	HEM4_BACSU	PUTATIVE UROPORPHYRINOGEN-III	130	6	6	3.65	0
20.	D35252	*Putative hemD protein - Baci	130	6	6	3.65	0
21.	P82320	PAP-III isolated from biologi	145	6	6	3.65	0
22.	JT0961	Glutathione synthase large ch	285	6	6	3.65	0
23.	CENA_MOUSE	CENTROSOMIN A.	289	6	6	3.65	0
24.	S13800	*Centrosomin A - Mouse	289	6	6	3.65	0
25.	R22403	Partial sequence of N-lipocor	304	6	6	3.65	0
26.	B41002	Annexin II (clones E4 and F4)	314	6	6	3.65	0
27.	R10689	Cephalosporin antibiotic bios	319	6	6	3.65	0
28.	ANX3_HUMAN	ANNEXIN III (LIPOCORTIN III)	323	6	6	3.65	0
29.	LUHU3	Annexin III - Human	323	6	6	3.65	0
30.	P91362	Human lipocortin-III.	323	6	6	3.65	0
31.	ANX3_RAT	ANNEXIN III (LIPOCORTIN III)	324	6	6	3.65	0
32.	LURT3	Annexin III - Rat	324	6	6	3.65	0
33.	VG16_BPPZA	ENCAPSIDATION PROTEIN (LATE P	332	6	6	3.65	0
34.	VG16_BPPH2	ENCAPSIDATION PROTEIN (LATE P	332	6	6	3.65	0
35.	JQ0168	Gene 16 protein - Phage phi-2	332	6	6	3.65	0
36.	WMBP26	Gene 16 protein - Phage phi-2	332	6	6	3.65	0
37.	WMBP16	Gene 16 protein - Phage PZA	332	6	6	3.65	0
38.	RIR2_HSV23	RIBONUCLEOSIDE-DIPHOSPHATE RE	337	6	6	3.65	0
39.	WMBEB2	Ribonucleoside-diphosphate re	337	6	6	3.65	0
40.	WMBE32	Ribonucleoside-diphosphate re	337	6	6	3.65	0
41.	ANX2_MOUSE	ANNEXIN II (LIPOCORTIN II) (C	338	6	6	3.65	0
42.	ANX2_HUMAN	ANNEXIN II (LIPOCORTIN II) (C	338	6	6	3.65	0
43.	ANX2_CHICK	ANNEXIN II (LIPOCORTIN II) (C	338	6	6	3.65	0
44.	ANX2_BOVIN	ANNEXIN II (LIPOCORTIN II) (C	338	6	6	3.65	0
45.	RIR2_HSV1K	RIBONUCLEOSIDE-DIPHOSPHATE RE	339	6	6	3.65	0
46.	ANXB_XENLA	ANNEXIN II TYPE I (LIPOCORTIN	339	6	6	3.65	0
47.	ANX2_XENLA	ANNEXIN II TYPE II (LIPOCORTI	339	6	6	3.65	0
48.	LUCH2	Annexin II - Chicken	339	6	6	3.65	0
49.	LUMS36	Annexin II - Mouse	339	6	6	3.65	0
50.	LUB036	Annexin II - Bovine	339	6	6	3.65	0

No alignments saved.

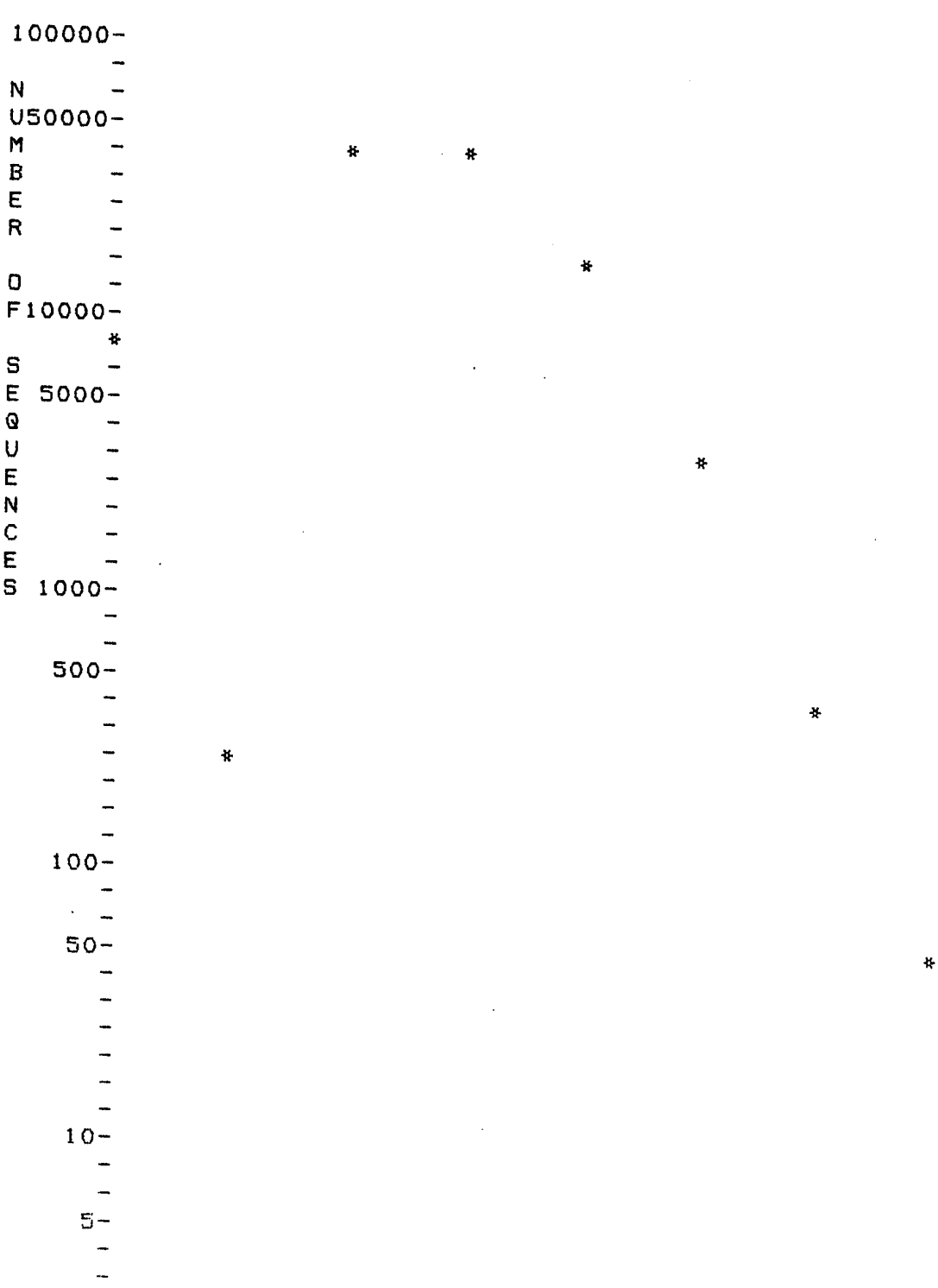
IntelliGenetics

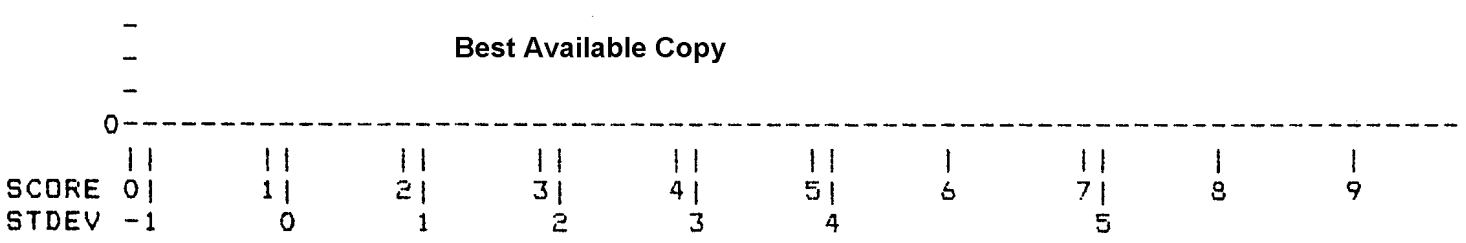
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-11.res made by alexk on Thu 25 Feb 93 10:24:30-PST.

Query sequence being compared: CELSA-11 (1-23)
Number of sequences searched: 94553
Number of scores above cutoff: 3948

Results of the initial comparison of CELSA-11 (1-23) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	4	1.13

Times:	CPU	Total Elapsed
	00:03:59.10	00:08:28.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 3948

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.
Cut-off raised to 6.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

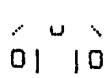
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 6 standard deviations above mean ****					
1. EFTU_EUGGR	ELONGATION FACTOR TU (EF-TU).	409	9	10	6.18	0
2. S02254	Elongation factor Tu - Euglen	409	9	10	6.18	0
3. EFEGT	Elongation factor Tu - Euglen	409	9	10	6.18	0
	**** 5 standard deviations above mean ****					
4. XYLR_STAXY	XYLOSE REPRESSOR.	383	8	8	5.29	0
5. S16529	*xylR protein - Staphylococcu	383	8	8	5.29	0
	**** 4 standard deviations above mean ****					
6. YDP3_LACLA	HYPOTHETICAL 18.0 KD PROTEIN	161	7	10	4.41	0
7. B33374	*Hypothetical protein BVRF1 -	193	7	9	4.41	0
8. YEIB_ECOLI	HYPOTHETICAL PROTEIN IN GALS	196	7	7	4.41	0
9. S19934	Hypothetical protein - Escher	196	7	7	4.41	0
10. UL52_HSVSA	HYPOTHETICAL BSLF1 PROTEIN HO	205	7	7	4.41	0
11. Q0BEHA	BSLF1 protein - Saimirine her	205	7	7	4.41	0
12. KAD_PARDE	ADENYLATE KINASE (EC 2.7.4.3)	217	7	7	4.41	0

14.	KIPC	Adenylate kinase - Paracoccus	217	7	7	4.41	0
15.	KAD1_YEAST	ADENYLATE KINASE CYTOSOLIC (E	222	7	8	4.41	0
16.	KIBYA	Adenylate kinase - Yeast (Sac	222	7	8	4.41	0
17.	R03339	VP1 sequence for HRV serotype	287	7	9	4.41	0
18.	R03340	VP1 sequence for HRV serotype	291	7	8	4.41	0
19.	CMG1_BACSU	COMG OPERON PROTEIN 1.	356	7	7	4.41	0
20.	B30338	*comG operon protein 1 - Baci	356	7	7	4.41	0
21.	RRPO_LYCVW	RNA POLYMERASE (EC 2.7.7.48)	363	7	9	4.41	0
22.	DDLA_ECOLI	D-ALANINE--D-ALANINE LIGASE A	364	7	7	4.41	0
23.	CEECDA	D-Alanine--D-alanine ligase A	364	7	7	4.41	0
24.	TRPB_ACICA	TRYPTOPHAN SYNTHASE BETA CHAI	403	7	8	4.41	0
25.	B36151	*Tryptophan synthase beta cha	403	7	8	4.41	0
26.	FIBG_BOVIN	FIBRINOGEN GAMMA-B CHAIN PREC	444	7	9	4.41	0
27.	S05313	Fibrinogen gamma-B chain prec	444	7	9	4.41	0
28.	FUCO_DICDI	ALPHA-L-FUCOSIDASE PRECURSOR	461	7	10	4.41	0
29.	A30364	alpha-L-Fucosidase homolog pr	461	7	10	4.41	0
30.	A41533	*Reticuline oxidase precursor	538	7	7	4.41	0
31.	VGNZPD	Fusion glycoprotein precursor	631	7	8	4.41	0
32.	NU5M_ASPNI	NADH-UBIQUINONE OXIDOREDUCTAS	657	7	8	4.41	0
33.	S04724	*NADH dehydrogenase (ubiquino	657	7	8	4.41	0
34.	UL15_HSV6U	HYPOTHETICAL PROTEIN 12L (ORF	667	7	9	4.41	0
35.	Q0BEH6	12L protein - Human herpesvir	667	7	9	4.41	0
36.	CAP1_HUMAN	CALPAIN I, LARGE (CATALYTIC)	714	7	9	4.41	0
37.	S10591	*Cysteine protease - Human	714	7	9	4.41	0
38.	CIHUH	Calpain I heavy chain - Human	714	7	9	4.41	0
39.	POLG_HRV1A	GENOME POLYPROTEIN (COAT PROT	832	7	9	4.41	0
40.	VCAP_HSV11	MAJOR CAPSID PROTEIN (MCP).	1374	7	7	4.41	0
41.	A30084	*Gene UL19 protein (major cap	1374	7	7	4.41	0
42.	VCBE17	Major capsid protein - Human	1374	7	7	4.41	0
43.	ARO1_YEAST	PENTAFUNCTIONAL AROM POLYPEPT	1588	7	8	4.41	0
44.	BVBYA1	ARO1 protein - Yeast (Sacchar	1588	7	8	4.41	0
45.	S18644	*Multifunctional aminoacyl-tR	1714	7	8	4.41	0
46.	RRPO_TACV	RNA POLYMERASE (EC 2.7.7.48).	2210	7	8	4.41	0
47.	RRXPTV	RNA-directed RNA polymerase -	2210	7	8	4.41	0
48.	S22011	*6-Deoxyerythronolide B synth	3567	7	8	4.41	0
49.	A41819	*637K proline-rich peptide pr	5762	7	9	4.41	0
		**** 3 standard deviations above mean ****					
50.	R15527	Immunopeptide derived from HP	20	6	6	3.53	0

No alignments saved.



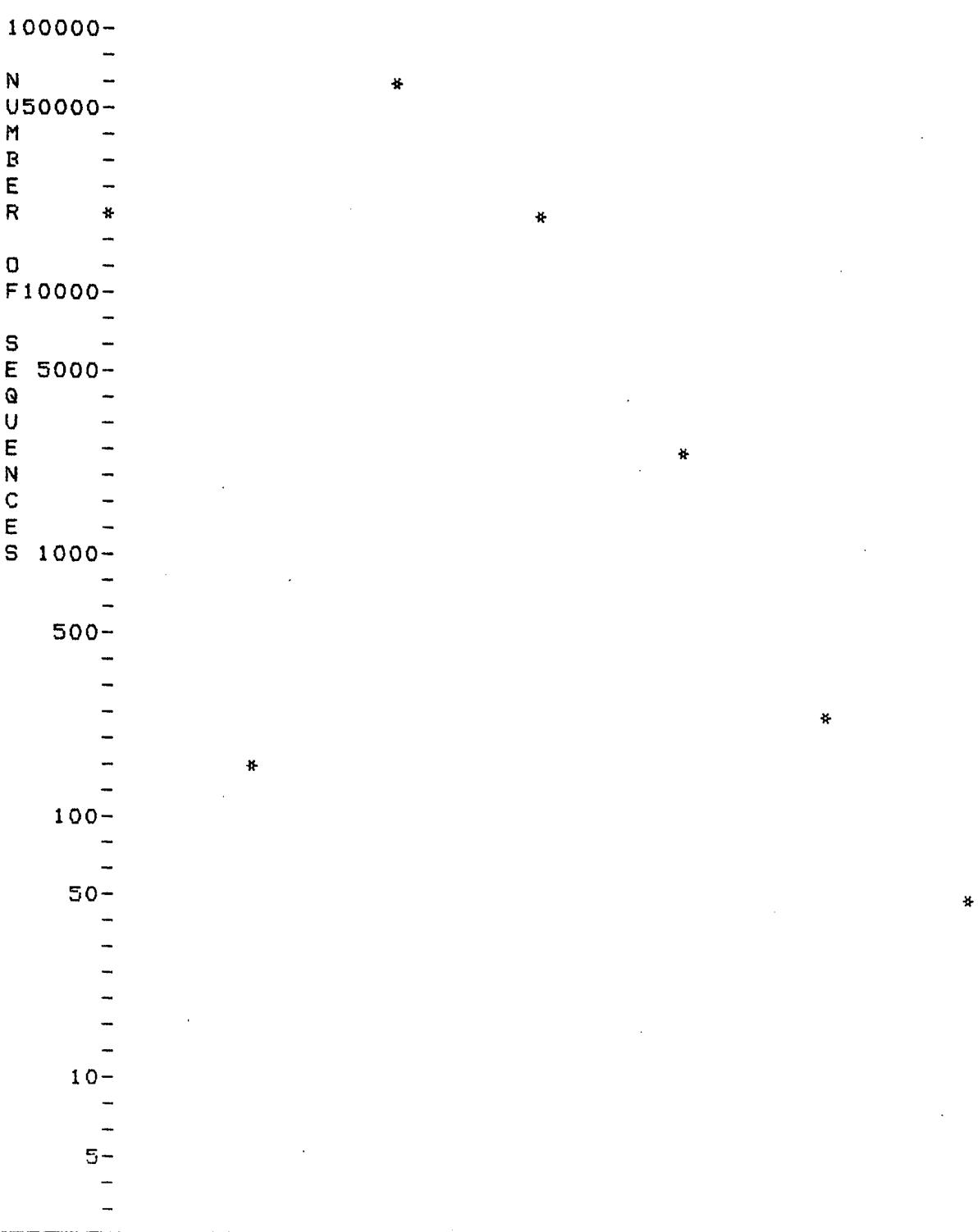
IntelliGenetics

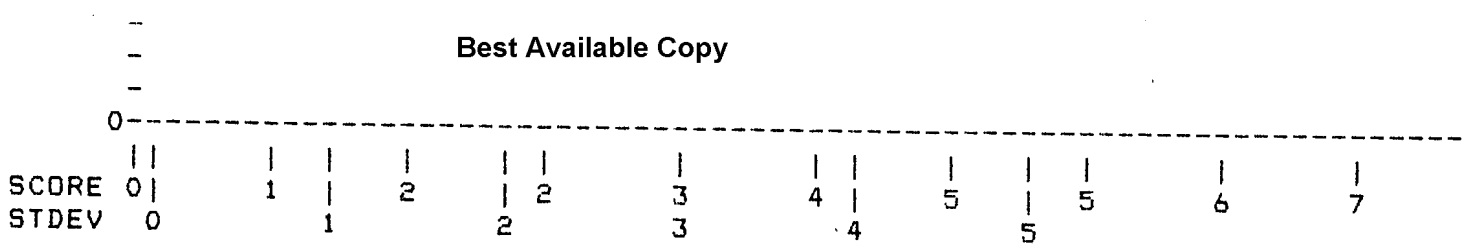
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-12.res made by alexk on Thu 25 Feb 93 10:32:32-PST.

Query sequence being compared: CELSA-12 (1-9)
Number of sequences searched: 94553
Number of scores above cutoff: 3845

Results of the initial comparison of CELSA-12 (1-9) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.04

Times:	CPU	Total Elapsed
	00:03:23.11	00:07:28.00

Number of residues:	25433612
Number of sequences searched:	94553
Number of scores above cutoff:	3845

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 5 standard deviations above mean ****					
1.	CYB_OENBE	CYTOCHROME B (EC 1.10.2.2).	394	7	7	5.76	0
2.	S20141	Cytochrome b - Evening primro	394	7	7	5.76	0
3.	CBOBE	Cytochrome b - Evening primro	394	7	7	5.76	0
		**** 4 standard deviations above mean ****					
4.	R13364	P691 HCV antigen (691-714).	24	6	6	4.80	0
5.	P92042	Sequence encoded in the hepat	141	6	6	4.80	0
6.	P90159	Sequence of hepatitis C virus	141	6	6	4.80	0
7.	S21305	*Apocytochrome b - Rice	334	6	6	4.80	0
8.	CYB_CHLSM	CYTOCHROME B (EC 1.10.2.2).	381	6	6	4.80	0
9.	CYB_CHLRE	CYTOCHROME B (EC 1.10.2.2).	381	6	6	4.80	0
10.	S12023	*Cytochrome b - Chlamydomonas	381	6	6	4.80	0
11.	S11966	*Cytochrome b - Chlamydomonas	381	6	6	4.80	0
12.	S12016	*Cytochrome b - Chlamydomonas	381	6	6	4.80	0
13.	CYB_MAIZE	CYTOCHROME B (EC 1.10.2.2).	388	6	6	4.80	0
14.	CBZM	Cytochrome b - Maize mitochon	388	6	6	4.80	0

16.	CBVF	Cytochrome b - Fava bean mito	392	6	6	4.80	0
17.	S17427	*Cytochrome b - Potato mitoch	393	6	6	4.80	0
18.	CYB_ORYSA	CYTOCHROME B (EC 1.10.2.2).	397	6	6	4.80	0
19.	S20659	*Apocytochrome b - Rice	397	6	6	4.80	0
20.	CBRZ	Cytochrome b - Rice mitochond	397	6	6	4.80	0
21.	CYB_WHEAT	CYTOCHROME B (EC 1.10.2.2).	398	6	6	4.80	0
22.	A22931	Cytochrome b - Wheat mitochon	398	6	6	4.80	0
23.	CYB_MARPO	CYTOCHROME B (EC 1.10.2.2).	404	6	6	4.80	0
24.	CARA_YEAST	CARBAMOYL-PHOSPHATE SYNTHASE,	411	6	6	4.80	0
25.	SYBYCS	Carbamoyl-phosphate synthase	411	6	6	4.80	0
26.	S20660	*Pseudo apocytochrome b - Ric	449	6	6	4.80	0
27.	P92049	Sequence encoded by segment o	454	6	6	4.80	0
28.	P90183	Sequence of hepatitis C virus	454	6	6	4.80	0
29.	R21577	HCV CKS-NS1 - pHCV-107.	467	6	6	4.80	0
30.	J01366	Polyprotein - Hepatitis C vir	716	6	6	4.80	0
31.	YCD9_YEAST	HYPOTHETICAL 86.0 KD PROTEIN	759	6	6	4.80	0
32.	S19367	Hypothetical protein YCL39W -	759	6	6	4.80	0
33.	P90164	Peptide encoded by composite	2261	6	6	4.80	0
34.	P92047	Sequence encoded in the hepat	2301	6	6	4.80	0
35.	P92050	Sequence encoded in the hepat	2436	6	6	4.80	0
36.	P90288	Peptide encoded by composite	2462	6	6	4.80	0
37.	R08123	Hepatitis C virus polypeptide	2772	6	6	4.80	0
38.	R24440	Composite HCV HC-J1/CDC/CHI p	2894	6	6	4.80	0
39.	R08124	Hepatitis C virus putative po	2955	6	6	4.80	0
40.	POLG_HCVH	GENOME POLYPROTEIN (CONTAINS:	3011	6	6	4.80	0
41.	POLG_HCV1	GENOME POLYPROTEIN (CONTAINS:	3011	6	6	4.80	0
42.	GNWVC3	Genome polyprotein - Hepatiti	3011	6	6	4.80	0
43.	R22154	NANBV Hutch c59 isolate genom	3011	6	6	4.80	0
44.	R21519	Compiled HCV sequence.	3011	6	6	4.80	0
		**** 3 standard deviations above mean ****					
45.	R15366	Ig idiotypic determinant PSL3	12	5	5	3.84	0
46.	R11408	Hepatitis B virus pre-S2 0E2-	38	5	5	3.84	0
47.	A24265	Phosphate transport protein,	47	5	5	3.84	0
48.	A25521	Ig kappa chain V region (321)	54	5	6	3.84	0
49.	S19988	*Hypothetical protein 1708 -	65	5	5	3.84	0
50.	S19981	*Hypothetical protein 1708 -	65	5	5	3.84	0

No alignments saved.

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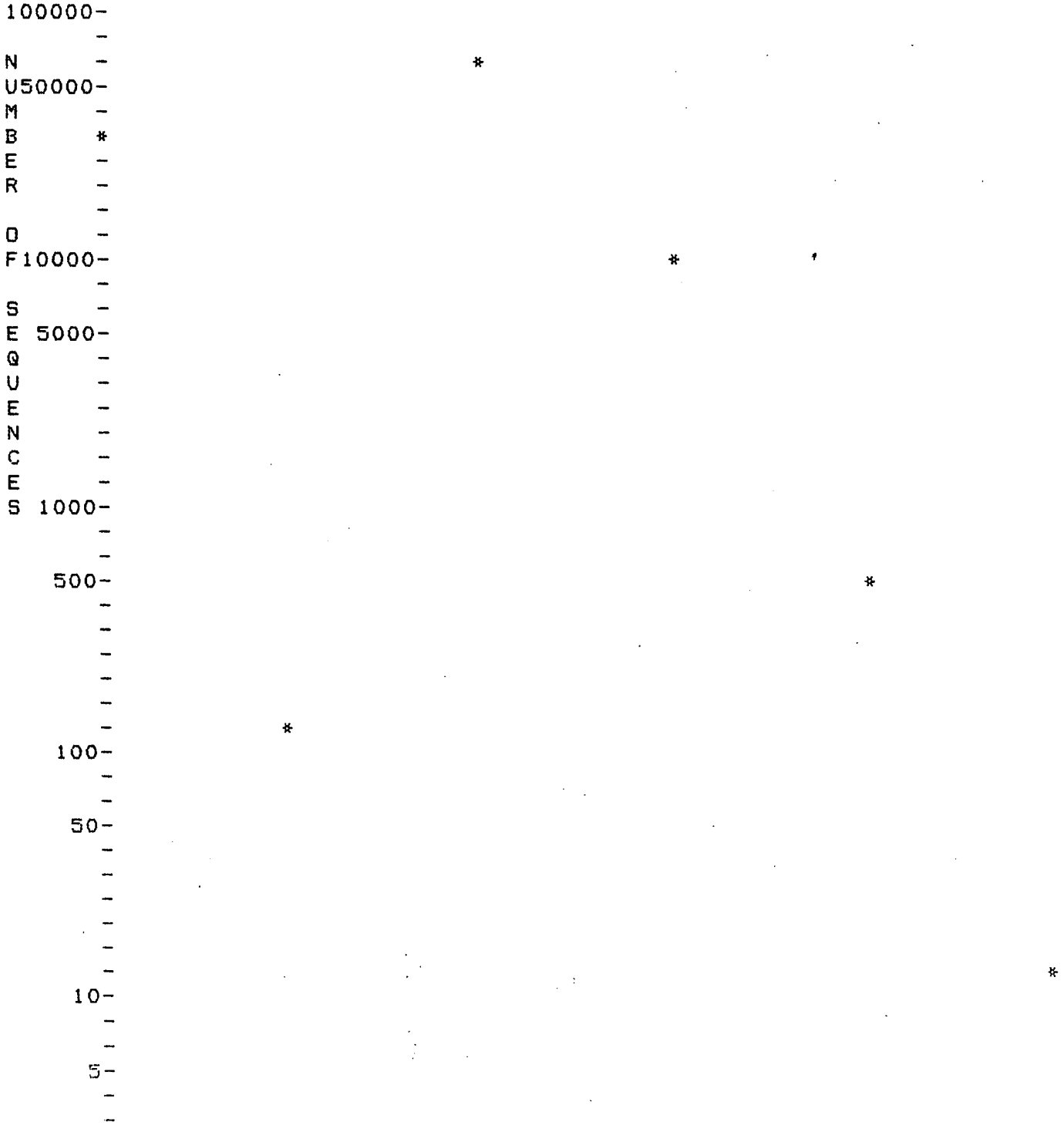
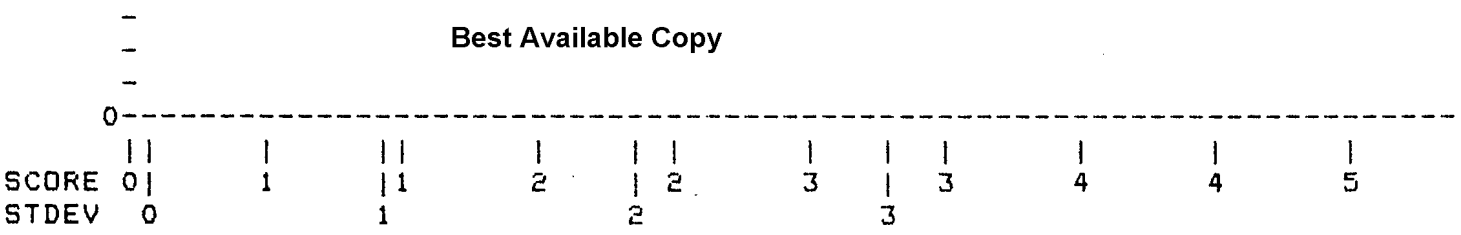
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-13.res made by alexk on Thu 25 Feb 93 10:39:48-PST.

Query sequence being compared: CELSA-13 (1-5)
Number of sequences searched: 94553
Number of scores above cutoff: 4106

Results of the initial comparison of CELSA-13 (1-5) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.01

Times:	CPU	Total Elapsed
	00:03:18.07	00:06:44.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4106

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

11 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	A37113	*Ryanodine receptor, cardiac	4969	5	5	3.98	0
2.	BVFFSL	sol protein, large splice for	1597	5	5	3.98	0
3.	SOL_DROME	SMALL OPTIC LOBES PROTEIN.	1597	5	5	3.98	0
4.	CP51_CANTR	CYTOCHROME P450 L1 (P450-L1A1	528	5	5	3.98	0
5.	A31854	Cytochrome P450 51 lanosterol	528	5	5	3.98	0
6.	S12042	*Sugar transport protein STP1	522	5	5	3.98	0
7.	STP1_ARATH	GLUCOSE TRANSPORTER (SUGAR CA	522	5	5	3.98	0
8.	S14627	*Glucose transport protein -	522	5	5	3.98	0
9.	B35901	*Calcium channel alpha-1 chai	164	5	5	3.98	0
10.	J00700	Hypothetical 11K protein (mmo	103	5	5	3.98	0
11.	YMM0_METCA	HYPOTHETICAL 11.9 KD PROTEIN	103	5	5	3.98	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
12.	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

14.	D24735	Glutathione transferase, 2-2	19	4	4	2.98	0
15.	A24735	Glutathione transferase, 1-1	26	4	4	2.98	0
16.	S21278	*Glutathione transferase chai	28	4	4	2.98	0
17.	S03358	*Glutathione transferase - Ra	31	4	4	2.98	0
18.	S09585	*Glutathione transferase - Ra	31	4	4	2.98	0
19.	V07K_PMV	7 KD PROTEIN (ORF 4).	68	4	4	2.98	0
20.	J00099	Hypothetical 7K protein - Pap	68	4	4	2.98	0
21.	P81053	Sequence of rhinovirus HRV2 v	69	4	4	2.98	0
22.	P81052	Sequence of rhinovirus HRV89	69	4	4	2.98	0
23.	TRAL_ECOLI	TRAL PROTEIN.	91	4	4	2.98	0
24.	BVECTL	traL protein - Escherichia co	91	4	4	2.98	0
25.	S03311	traL protein - Escherichia co	92	4	4	2.98	0
26.	VE5_HPV42	PROBABLE E5 PROTEIN.	95	4	4	2.98	0
27.	W5WL42	E5 protein - Human papillomav	95	4	4	2.98	0
28.	YR12_CYAPA	HYPOTHETICAL 12.3 KD PROTEIN	102	4	4	2.98	0
29.	S12809	Hypothetical protein (rpl3 5'	102	4	4	2.98	0
30.	S14355	*Glutathione transferase - Ra	113	4	4	2.98	0
31.	THIO_ANASP	THIOREDOXIN.	115	4	4	2.98	0
32.	A32233	*Thioredoxin - Anabaena sp.	115	4	4	2.98	0
33.	VG67_BPPZA	EARLY PROTEIN GP16.7.	130	4	4	2.98	0
34.	VG67_BPPH5	EARLY PROTEIN GP16.7.	130	4	4	2.98	0
35.	VG67_BPPH2	EARLY PROTEIN GP16.7.	130	4	4	2.98	0
36.	JN0033	Early protein gp15 - Phage ph	130	4	4	2.98	0
37.	WRBPF5	Early protein gp15 - Phage ph	130	4	4	2.98	0
38.	WRBP67	Early protein gp15 - Phage PZ	130	4	4	2.98	0
39.	YKP7_KLULA	HYPOTHETICAL KILLER PLASMID P	132	4	4	2.98	0
40.	S15966	*Hypothetical protein 7 - Yea	132	4	4	2.98	0
41.	S00965	Hypothetical protein 7 - Yeas	132	4	4	2.98	0
42.	S19269	*Glutathione transferase Yc2	139	4	4	2.98	0
43.	BCP_ECOLI	BACTERIOFERRITIN COMIGRATORY	156	4	4	2.98	0
44.	V02_FMVD	PROTEIN 2.	164	4	4	2.98	0
45.	S01280	Hypothetical protein 2 - Figw	164	4	4	2.98	0
46.	NU6M_MOUSE	NADH-UBIQUINONE OXIDOREDUCTAS	172	4	4	2.98	0
47.	DEMSN6	NADH dehydrogenase (ubiquinon	172	4	4	2.98	0
48.	PSP_BOVIN	PANCREATIC STONE PROTEIN PREC	175	4	4	2.98	0
49.	A37194	*Pancreatic thread protein pr	175	4	4	2.98	0
50.	JS0679	Hypothetical 20K protein - Hu	175	4	4	2.98	0

No alignments saved.

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-14.res made by alexk on Thu 25 Feb 93 10:28:57-PST.


Query sequence being compared:       CELSA-14 (1-5)
Number of sequences searched:                94553
Number of scores above cutoff:                4598

      Results of the initial comparison of CELSA-14 (1-5) with:
   Data bank : A-GeneSeq 9, all entries
   Data bank : PIR 34, all entries
   Data bank : Swiss-Prot 23, all entries

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M      -
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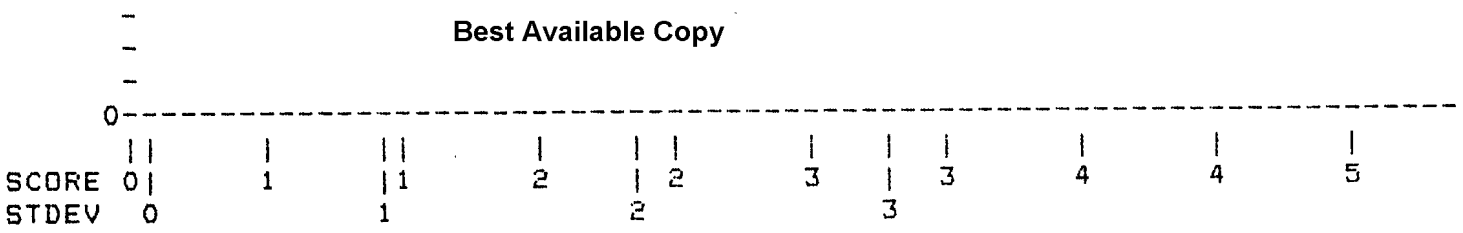

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.05

Times:	CPU	Total Elapsed
	00:03:18.06	00:06:52.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4598

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

too many to printout completly I've printed the 1st 20 only

145 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	S18268	*alpha-Aminoadipyl-L-cysteiny	3649	5	5	3.82	0
2.	ACVS_NOCLA	L-(ALPHA-AMINOADIPYL)-L-CYSTE	3649	5	5	3.82	0
3.	S12332	Ubiquitin--protein ligase - Y	1950	5	5	3.82	0
4.	UBR1_YEAST	N-END-RECOGNIZING PROTEIN (UB	1950	5	5	3.82	0
5.	RRWGNV	RNA-directed RNA polymerase -	1643	5	5	3.82	0
6.	VOR1_NMV	186 KD PROTEIN (ORF 1).	1643	5	5	3.82	0
7.	WMWGPV	RNA-directed RNA polymerase -	1456	5	5	3.82	0
8.	S14005	*Hypothetical protein, 166K -	1456	5	5	3.82	0
9.	VOR1_PVX	165 KD PROTEIN (ORF 1).	1456	5	5	3.82	0
10.	VOR1_PVXCP	165 KD PROTEIN (ORF 1).	1456	5	5	3.82	0
11.	VOR1_PVXX3	165 KD PROTEIN (ORF 1).	1456	5	5	3.82	0
12.	VGIHJ2	E2 glycoprotein precursor - M	1376	5	5	3.82	0
13.	VGL2_CVM4	E2 GLYCOPROTEIN PRECURSOR (SP	1376	5	5	3.82	0
14.	VGIH59	E2 glycoprotein precursor - M	1324	5	5	3.82	0
15.	VGL2_CVMA5	E2 GLYCOPROTEIN PRECURSOR (SP	1324	5	5	3.82	0
16.	VGIHMJ	E2 glycoprotein precursor - M	1235	5	5	3.82	0
17.	VGL2_CVMJH	E2 GLYCOPROTEIN PRECURSOR (SP	1235	5	5	3.82	0
18.	A40986	*M-cadherin - Mouse (fragment	730	5	5	3.82	0
19.	SAHUAE	Cell surface antigen 4F2 heav	529	5	5	3.82	0

21.	A37959	*Cell surface antigen 4F2 hea	529	5	5	3.82	0
22.	4F2_HUMAN	4F2 CELL-SURFACE ANTIGEN HEAV	529	5	5	3.82	0
23.	S20477	Ribulose-bisphosphate carboxy	498	5	5	3.82	0
24.	RKFPLP	Ribulose-bisphosphate carboxy	485	5	5	3.82	0
25.	RKFPLB	Ribulose-bisphosphate carboxy	485	5	5	3.82	0
26.	D34921	*Ribulose-bisphosphate carbox	485	5	5	3.82	0
27.	RBL_FLABI	RIBULOSE BISPHOSPHATE CARBOXY	485	5	5	3.82	0
28.	C34921	*Ribulose-bisphosphate carbox	485	5	5	3.82	0
29.	RBL_FLAPR	RIBULOSE BISPHOSPHATE CARBOXY	485	5	5	3.82	0
30.	RBL_PHYAM	RIBULOSE BISPHOSPHATE CARBOXY	482	5	5	3.82	0
31.	RBL_STEHA	RIBULOSE BISPHOSPHATE CARBOXY	482	5	5	3.82	0
32.	RBL_ALLPR	RIBULOSE BISPHOSPHATE CARBOXY	480	5	5	3.82	0
33.	S20847	*Ribulose-bisphosphate carbox	480	5	5	3.82	0
34.	RBL_BASAL	RIBULOSE BISPHOSPHATE CARBOXY	480	5	5	3.82	0
35.	RBL_MOLVE	RIBULOSE BISPHOSPHATE CARBOXY	480	5	5	3.82	0
36.	RBL_RIVHU	RIBULOSE BISPHOSPHATE CARBOXY	480	5	5	3.82	0
37.	RBL_TRIPO	RIBULOSE BISPHOSPHATE CARBOXY	480	5	5	3.82	0
38.	RKNULT	Ribulose-bisphosphate carboxy	478	5	5	3.82	0
39.	G34921	*Ribulose-bisphosphate carbox	478	5	5	3.82	0
40.	RBL_NEUMU	RIBULOSE BISPHOSPHATE CARBOXY	478	5	5	3.82	0
41.	RBL_NEUTE	RIBULOSE BISPHOSPHATE CARBOXY	478	5	5	3.82	0
42.	RKNULM	Ribulose-bisphosphate carboxy	478	5	5	3.82	0
43.	H34921	*Ribulose-bisphosphate carbox	478	5	5	3.82	0
44.	P50585	Maize ribulose-biphosphate ca	477	5	5	3.82	0
45.	RKNTLO	Ribulose-bisphosphate carboxy	477	5	5	3.82	0
46.	RKNTLA	Ribulose-bisphosphate carboxy	477	5	5	3.82	0
47.	RKRZL	Ribulose-bisphosphate carboxy	477	5	5	3.82	0
48.	RBL_NICAC	RIBULOSE BISPHOSPHATE CARBOXY	477	5	5	3.82	0
49.	RBL_NICOT	RIBULOSE BISPHOSPHATE CARBOXY	477	5	5	3.82	0
50.	RBL_ORYSA	RIBULOSE BISPHOSPHATE CARBOXY	477	5	5	3.82	0

No alignments saved.

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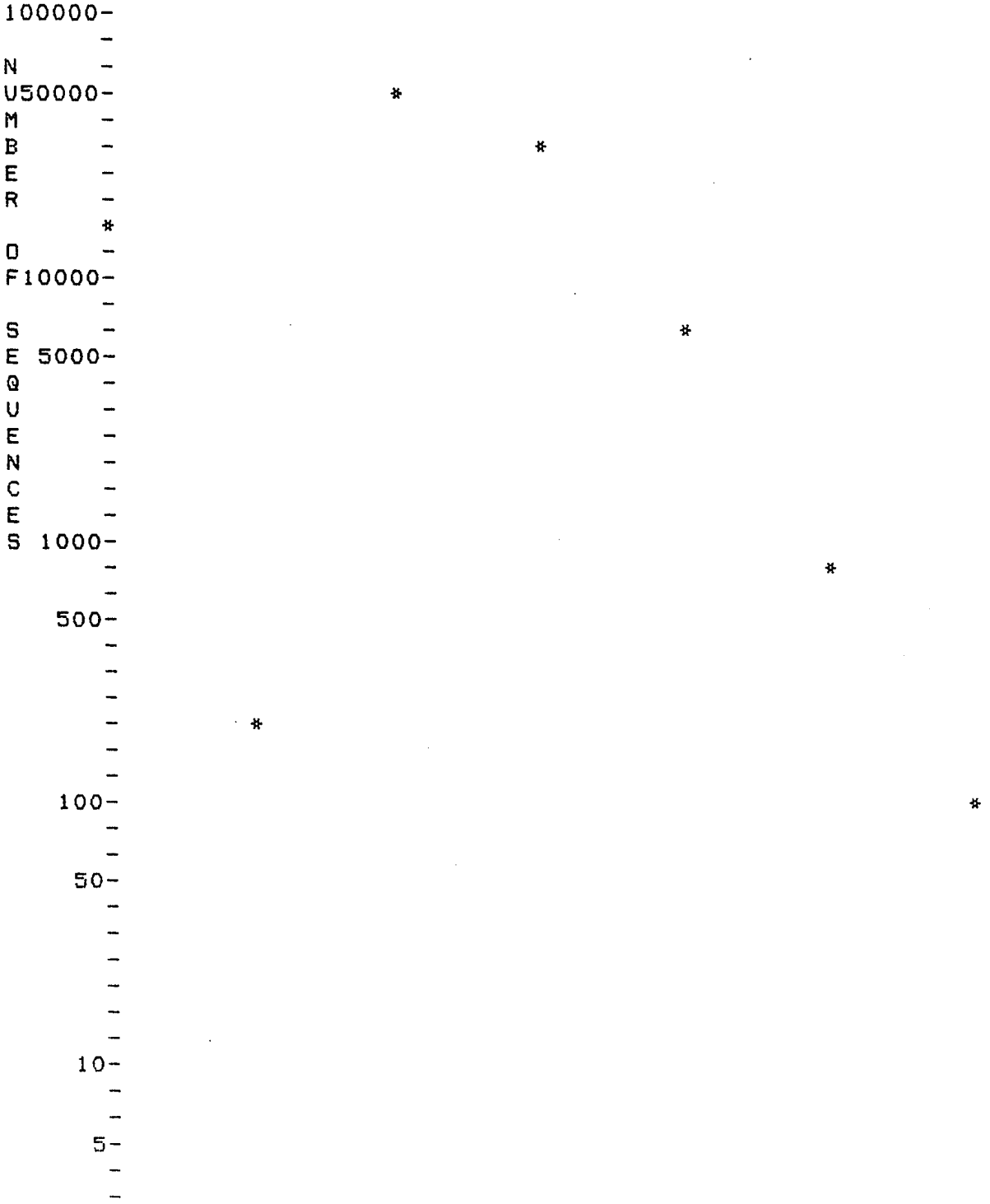
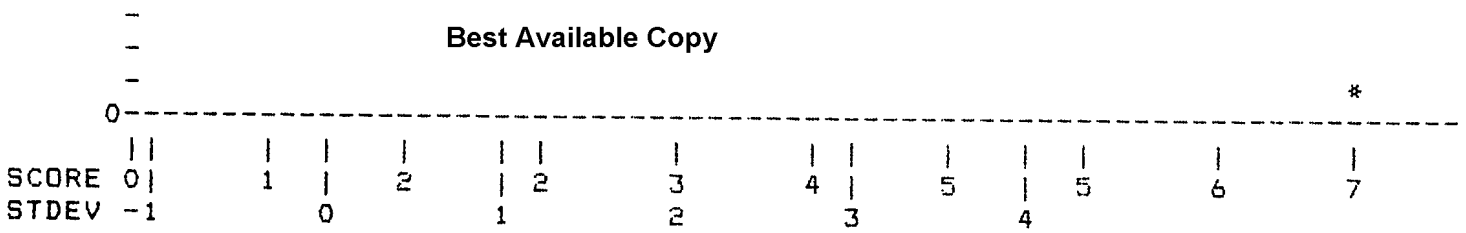
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-15.res made by alexk on Thu 25 Feb 93 10:45:14-PST.

Query sequence being compared: CELSA-15 (1-11)
Number of sequences searched: 94553
Number of scores above cutoff: 4356

Results of the initial comparison of CELSA-15 (1-11) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:

Mean	Median	Standard Deviation
2	3	1.06

Times:

CPU	Total Elapsed
00:03:32.04	00:07:11.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4356

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 4 standard deviations above mean ****					
1. DP3B_STRCO	DNA POLYMERASE III, BETA CHAI	376	7	7	4.71	0
	**** 3 standard deviations above mean ****					
2. UL96_HCMVA	HYPOTHETICAL PROTEIN UL96.	115	6	6	3.77	0
3. S09861	Hypothetical protein UL96 - H	115	6	6	3.77	0
4. FKBP_NEUCR	FK506-BINDING PROTEIN (FKBP)	120	6	6	3.77	0
5. S11090	*FK506-binding protein - Neur	120	6	6	3.77	0
6. P00185	Tonoplast intrinsic protein b	169	6	6	3.77	0
7. POL_SFV1	POL POLYPROTEIN (REVERSE TRAN	193	6	7	3.77	0
8. A33562	*pol polyprotein - Simian foa	193	6	7	3.77	0
9. S05586	Hypothetical protein 2 - Maiz	216	6	6	3.77	0
10. A41378	*Hypothetical protein (cycB 5	221	6	6	3.77	0
11. A05182	Alcohol dehydrogenase beta -	243	6	6	3.77	0
12. A31087	Alzheimer's disease amyloid b	264	6	6	3.77	0
13. P90609	Sequence of amy 37 clone.	264	6	6	3.77	0
14. P90497	Protein sequence including th	274	6	6	3.77	0

16. KPR2_HUMAN	RIBOSE-PHOSPHATE PYROPHOSPHOK	317	6	6	3.77	0
17. KPR1_HUMAN	RIBOSE-PHOSPHATE PYROPHOSPHOK	317	6	6	3.77	0
18. KIRTR1	Ribose-phosphate pyrophosphok	318	6	6	3.77	0
19. KIHUR1	Ribose-phosphate pyrophosphok	318	6	6	3.77	0
20. KIRTR2	Ribose-phosphate pyrophosphok	318	6	6	3.77	0
21. KIHUR2	Ribose-phosphate pyrophosphok	318	6	6	3.77	0
22. COBD_PSEDE	COBD PROTEIN.	323	6	6	3.77	0
23. E36144	*cobD protein - Pseudomonas s	323	6	6	3.77	0
24. R13495	P.denitrificans COB D.	323	6	6	3.77	0
25. CELF_HSV2H	CELL FUSION PROTEIN PRECURSOR	338	6	6	3.77	0
26. JH0143	Syn protein - Human herpesvir	338	6	6	3.77	0
27. YT44_STRFR	HYPOTHETICAL 44.4 KD PROTEIN	395	6	6	3.77	0
28. JQ0430	Hypothetical 44.4K protein -	395	6	6	3.77	0
29. A30320	*Alzheimer's disease amyloid	412	6	6	3.77	0
30. A29030	Alzheimer's disease amyloid A	412	6	6	3.77	0
31. NCAP_DUGBV	NUCLEOCAPSID PROTEIN (NUCLEOP	441	6	6	3.77	0
32. VHVUDU	Nucleocapsid protein N - Dugb	441	6	6	3.77	0
33. A32761	*Alzheimer's disease amyloid	484	6	6	3.77	0
34. GAG_HIV1U	GAG POLYPROTEIN (CORE PROTEIN	493	6	6	3.77	0
35. GAG_HIV1N	GAG POLYPROTEIN (CORE PROTEIN	500	6	6	3.77	0
36. P91256	Recombinant gag precursor of	500	6	6	3.77	0
37. OCTC_RAT	CARNITINE OCTANOYLTRANSFERASE	523	6	6	3.77	0
38. A31948	Carnitine octanoyltransferase	523	6	6	3.77	0
39. B30320	*Alzheimer's disease amyloid	574	6	6	3.77	0
40. UL32_HSV11	HYPOTHETICAL PROTEIN UL32.	596	6	6	3.77	0
41. WMBEH2	UL32 protein - Human herpesvi	596	6	6	3.77	0
42. HEMA_MEASH	HEMAGGLUTININ-NEURAMINIDASE (	617	6	6	3.77	0
43. HEMA_MEASE	HEMAGGLUTININ-NEURAMINIDASE (	617	6	6	3.77	0
44. HMNZED	Hemagglutinin - Measles virus	617	6	6	3.77	0
45. HMNZHA	Hemagglutinin - Measles virus	617	6	6	3.77	0
46. HEMA_MEASY	HEMAGGLUTININ-NEURAMINIDASE (	620	6	6	3.77	0
47. JU0273	Hemagglutinin - Measles virus	620	6	6	3.77	0
48. S18607	*Phosphotransferase system en	651	6	6	3.77	0
49. B41080	*Probable transketolase - Rho	657	6	6	3.77	0
50. A4_RAT	ALZHEIMER'S DISEASE AMYLOID A	695	6	6	3.77	0

No alignments saved.

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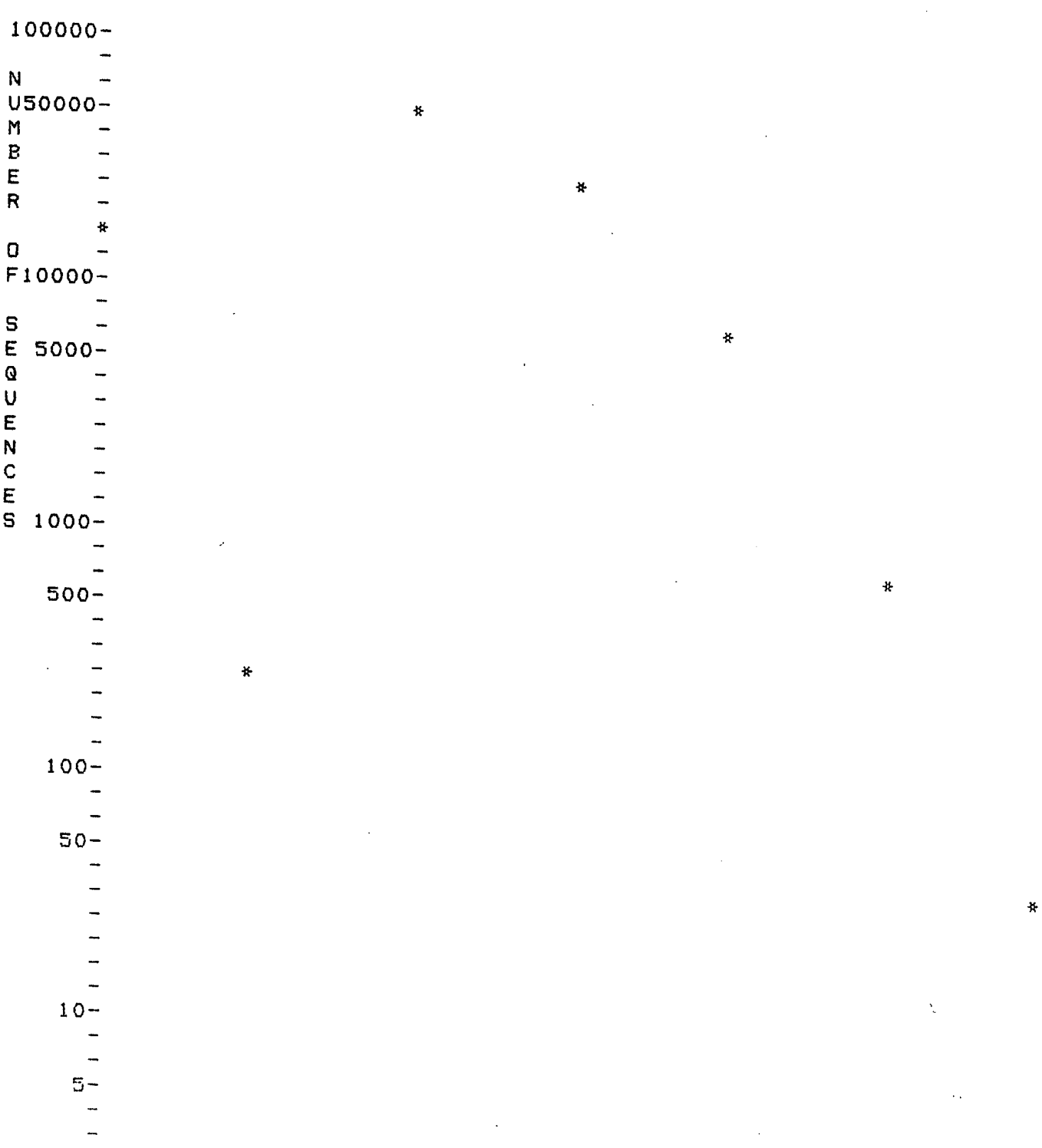
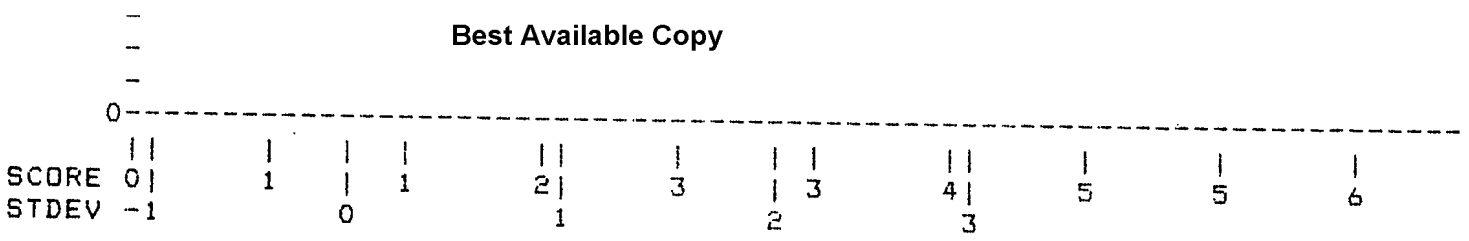
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-16.res made by alexk on Thu 25 Feb 93 10:45:14-PST.

Query sequence being compared: CELSA-16 (1-11)
Number of sequences searched: 94553
Number of scores above cutoff: 4223

Results of the initial comparison of CELSA-16 (1-11) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:

Mean	Median	Standard Deviation
2	3	1.08

Times:

CPU	Total Elapsed
00:03:26.11	00:07:10.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4223

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 3 standard deviations above mean ****					
1.	PE25_NPVAC	25.1 KD PROTEIN IN PE-P26 INT	219	6	6	3.71	0
2.	NTRB_VIBAL	NITROGEN REGULATION PROTEIN N	350	6	7	3.71	0
3.	JL0114	ntrB protein - Vibrio alginol	350	6	7	3.71	0
4.	GUN_CELUD	ENDOGLUCANASE PRECURSOR (EC 3	359	6	6	3.71	0
5.	P70396	Cellulase.	359	6	6	3.71	0
6.	IL1S_HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE	398	6	6	3.71	0
7.	S17428	*Interleukin-1 receptor, type	398	6	6	3.71	0
8.	R15614	Human type II interleukin-1 r	398	6	6	3.71	0
9.	R12786	Actinomycete Phospholipase D.	524	6	6	3.71	0
10.	UL32_EBV	HYPOTHETICAL PROTEIN BFLF1.	525	6	6	3.71	0
11.	Q0BE6	BFLF1 protein - Human herpesv	525	6	6	3.71	0
12.	SPG7_DICDI	SPORE GERMINATION PROTEIN 270	532	6	6	3.71	0
13.	B35621	Spore germination protein 270	532	6	6	3.71	0
14.	VGLE_HSV11	GLYCOPROTEIN E PRECURSOR.	550	6	6	3.71	0
15.	VGBE18	Glycoprotein E - Human herpes	550	6	6	3.71	0

17.	S19202	*Glycoprotein Ben precursor -	588	6	7	3.71	0
18.	JH0506	Adhesion molecule SC1 precurs	588	6	7	3.71	0
19.	JH0593	Schwann cell myelin protein p	620	6	6	3.71	0
20.	VP3_RDV	MAJOR 114 KD STRUCTURAL PROTE	1019	6	6	3.71	0
21.	S12826	*Hypothetical protein - Rice	1019	6	6	3.71	0
22.	S12621	*114K major core protein - Ri	1019	6	6	3.71	0
23.	S20548	*P-glycoprotein homolog - Yea	1362	6	6	3.71	0
24.	KRE5_YEAST	KRE5 PROTEIN PRECURSOR.	1365	6	6	3.71	0
25.	BVBYK5	KRE5 protein precursor - Yeas	1365	6	6	3.71	0
26.	A39401	*Merozoite surface antigen 1	1726	6	6	3.71	0
27.	TEGU_VZVD	LARGE TEGUMENT PROTEIN.	2763	6	6	3.71	0
28.	WZBE22	Gene 22 protein - Human herpe	2763	6	6	3.71	0
		**** 2 standard deviations above mean ****					
29.	R12065	Antigenic peptide #2269 D5/19	15	5	5	2.78	0
30.	S11617	Ribosomal protein HS17 - Halo	30	5	5	2.78	0
31.	S19945	Protein kinase crk3 - Mouse (	35	5	5	2.78	0
32.	P91884	Antigenic Epstein-Barr virus	48	5	5	2.78	0
33.	S02383	Probable membrane antigen CL3	57	5	5	2.78	0
34.	C27606	Ig heavy chain V-a region (p2	58	5	5	2.78	0
35.	S22133	*Hypothetical protein - Esche	76	5	5	2.78	0
36.	KPSJ_HUMAN	PUTATIVE SERINE/THREONINE-PRO	101	5	5	2.78	0
37.	C26368	Protein-serine kinase (clone	101	5	5	2.78	0
38.	NRAM_IADA1	NEURAMINIDASE (EC 3.2.1.18) (	103	5	6	2.78	0
39.	CYTA_RAT	CYSTATIN ALPHA (EPIDERMAL THI	103	5	5	2.78	0
40.	A00891	Sialidase - Influenza A virus	103	5	6	2.78	0
41.	UDRTS2	Cystatin alpha - Rat	103	5	5	2.78	0
42.	HM20_XENLA	HOMEOTIC PROTEIN NRL-20 (FRAG	105	5	5	2.78	0
43.	S12181	*Xl-pou protein - African cla	105	5	5	2.78	0
44.	S21856	*Collagen alpha 1(X) chain -	106	5	5	2.78	0
45.	S15826	*Collagen - Human	106	5	5	2.78	0
46.	KV6K_MOUSE	IG KAPPA CHAIN V-VI REGION (N	108	5	5	2.78	0
47.	PRVA_RAJCL	PARVALBUMIN ALPHA.	109	5	5	2.78	0
48.	S11125	*Ig heavy chain V region - Mo	109	5	5	2.78	0
49.	PVRYC	Parvalbumin - Thornback ray	109	5	5	2.78	0
50.	P70092	Sequence encoded by (2'-5') o	110	5	6	2.78	0

No alignments saved.

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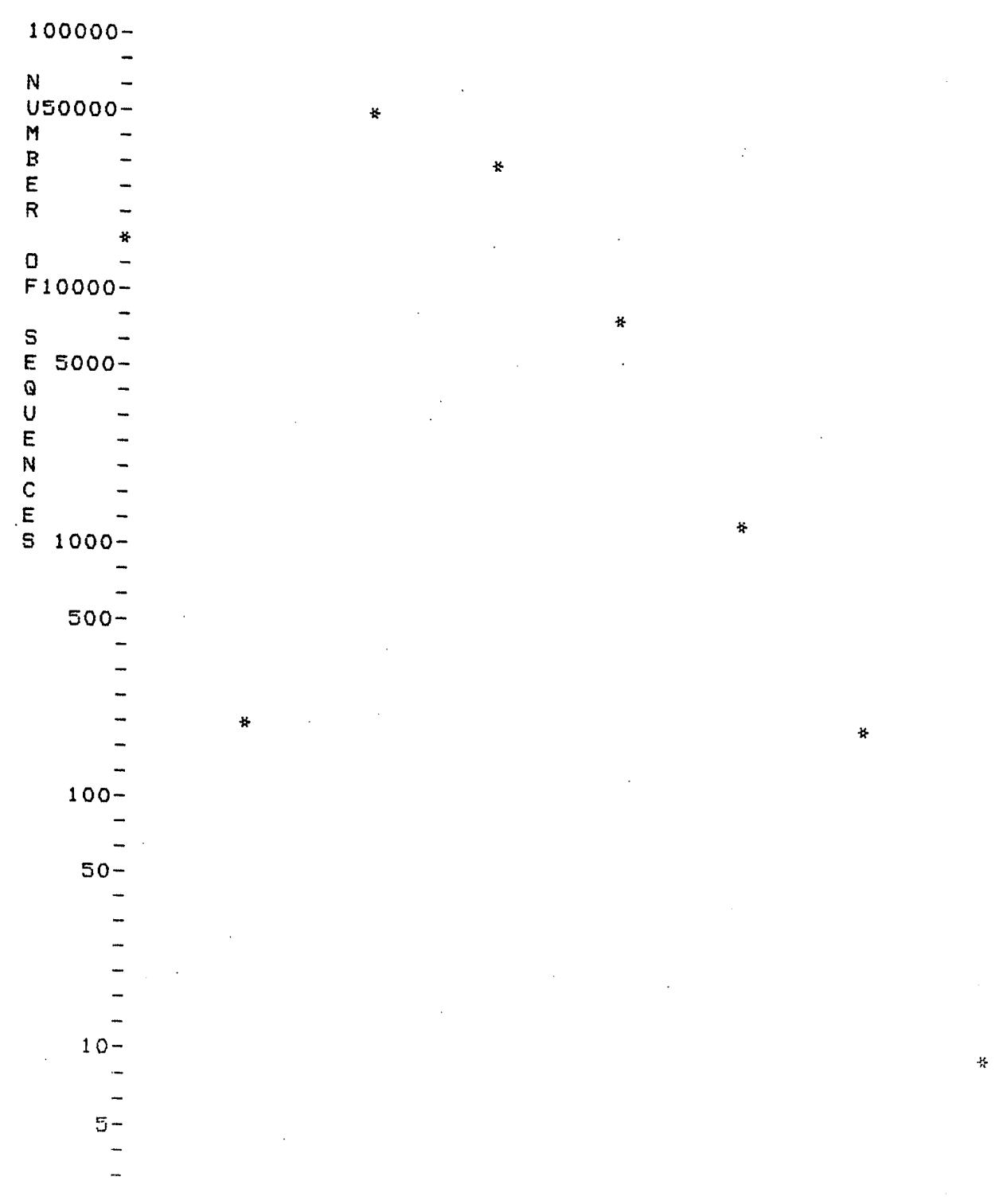
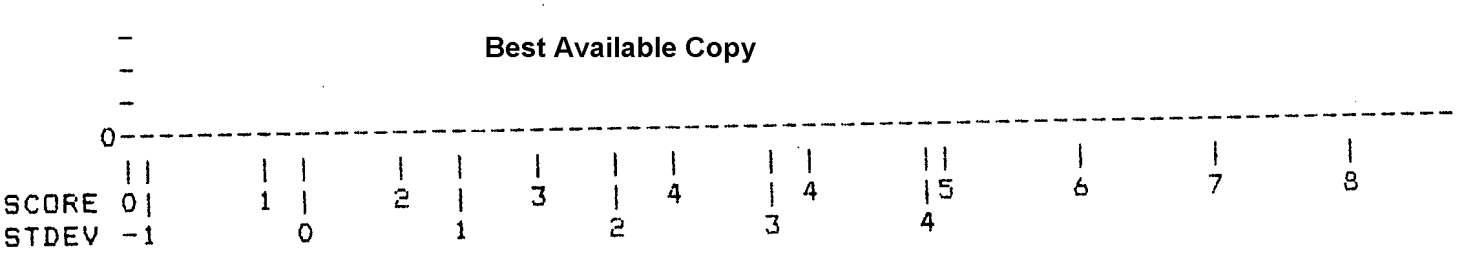
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-17.res made by alexk on Thu 25 Feb 93 10:29:14-PST.

Query sequence being compared: CELSA-17 (1-13)
Number of sequences searched: 94553
Number of scores above cutoff: 4785

Results of the initial comparison of CELSA-17 (1-13) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	3	1.13

Times:	CPU	Total Elapsed
	00:03:37.03	00:07:11.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4785

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 5 standard deviations above mean ****					
1. LV4A_HUMAN	IG LAMBDA CHAIN V-IV REGION (	106	8	8	5.32	0
2. L4HUBU	Ig lambda chain V-IV region (	106	8	8	5.32	0
	**** 4 standard deviations above mean ****					
3. HMN3_DROME	HOMEOBOX PROTEIN NK-3 (FRAGME	194	7	7	4.43	0
4. C33976	*NK-3 homeotic protein - Frui	194	7	7	4.43	0
5. ATP6_STRPU	ATP SYNTHASE A CHAIN (EC 3.6.	229	7	7	4.43	0
6. S01505	H+-transporting ATP synthase	229	7	7	4.43	0
7. TRPD_BACSU	ANTHRANILATE PHOSPHORIBOSYLTR	337	7	7	4.43	0
8. B22794	Anthranilate phosphoribosyltr	337	7	7	4.43	0
9. NPBS	Anthranilate phosphoribosyltr	337	7	7	4.43	0
10. TRPD_BACPU	ANTHRANILATE PHOSPHORIBOSYLTR	340	7	7	4.43	0
11. JH0099	trpD protein - Bacillus pumil	340	7	7	4.43	0
	**** 3 standard deviations above mean ****					
12. A31093	Stage IV sporulation protein	43	6	6	3.55	0
	*NK-3 homeotic protein - M	60	6	6	3.55	0

15.	[illegible]	*Hox 2.4 homeotic protein - M	62	6	6	3.55	0
16.	V7K_BYDVP	6.7 KD PROTEIN (ORF 5).	63	6	6	3.55	0
17.	S00951	Hypothetical protein, 6.7K -	63	6	6	3.55	0
18.	S15534	Homeotic protein Hox 3A - Hum	66	6	6	3.55	0
19.	S15533	Homeotic protein Hox 2D - Hum	66	6	6	3.55	0
20.	S13785	*Homeotic protein m31 - Mouse	69	6	6	3.55	0
21.	HM24_HUMAN	HOMEOBOX PROTEIN HOX-2.4 (HOX	70	6	6	3.55	0
22.	B37042	*Homeotic protein Hox 2.4 - H	70	6	6	3.55	0
23.	NU4M_ARTSX	NADH-UBIQUINONE OXIDOREDUCTAS	71	6	8	3.55	0
24.	S01211	NADH dehydrogenase (ubiquinon	71	6	8	3.55	0
25.	HM24_CHICK	HOMEOBOX PROTEIN CHOX-2.4 (FR	74	6	6	3.55	0
26.	S10884	*Homeotic protein Hox 2.4 - C	74	6	6	3.55	0
27.	S14975	*Extensin class II - Tomato	82	6	6	3.55	0
28.	HM54_HUMAN	HOMEOBOX PROTEIN HOX-5.4 (HOX	95	6	6	3.55	0
29.	B32830	*Hox5.4 homeotic protein - Hu	95	6	6	3.55	0
30.	S05957	Homeotic protein Hox 4E - Hum	95	6	6	3.55	0
31.	YENM_SALTY	HYPOTHETICAL 10.4 KD PROTEIN	99	6	6	3.55	0
32.	S15521	*Homeotic protein Hox 4.3 - M	99	6	6	3.55	0
33.	S16177	*Homeotic protein Hox 4.3 - M	99	6	6	3.55	0
34.	HMR4_RAT	HOMEOBOX PROTEIN R4 (FRAGMENT	104	6	6	3.55	0
35.	HMRA_RAT	HOMEOBOX PROTEIN R1A (FRAGMEN	114	6	6	3.55	0
36.	KV3J_HUMAN	IG KAPPA CHAIN PRECURSOR V-II	116	6	6	3.55	0
37.	K3HUVH	Ig kappa chain precursor V-II	116	6	6	3.55	0
38.	R15106	hCG/bLH chimera, D10	145	6	6	3.55	0
39.	NODN_RHIME	NODULATION PROTEIN N.	160	6	6	3.55	0
40.	S16566	*nolN protein - Rhizobium mel	160	6	6	3.55	0
41.	IT1B_PSOTE	TRYPSIN INHIBITOR 1B (WTI-1B)	172	6	6	3.55	0
42.	IT1A_PSOTE	TRYPSIN INHIBITOR 1A (WTI-1A)	172	6	6	3.55	0
43.	TIWDKB	Trypsin inhibitor 1B (Kunitz)	172	6	6	3.55	0
44.	TIWDK	Trypsin inhibitor 1A (Kunitz)	172	6	6	3.55	0
45.	FRI3_RANCA	FERRITIN, LOWER SUBUNIT (FERR	173	6	7	3.55	0
46.	B27805	Ferritin chain L - Bullfrog	174	6	7	3.55	0
47.	CRTZ_ERWUR	CRTZ PROTEIN (EC -.-.-.-).	175	6	6	3.55	0
48.	F37802	*crtZ protein - Erwinia uredo	175	6	6	3.55	0
49.	R07468	Polypeptide with enzymatic ac	175	6	6	3.55	0
50.	IT2_PSOTE	TRYPSIN INHIBITOR 2 (WTI-2).	182	6	6	3.55	0

No alignments saved.

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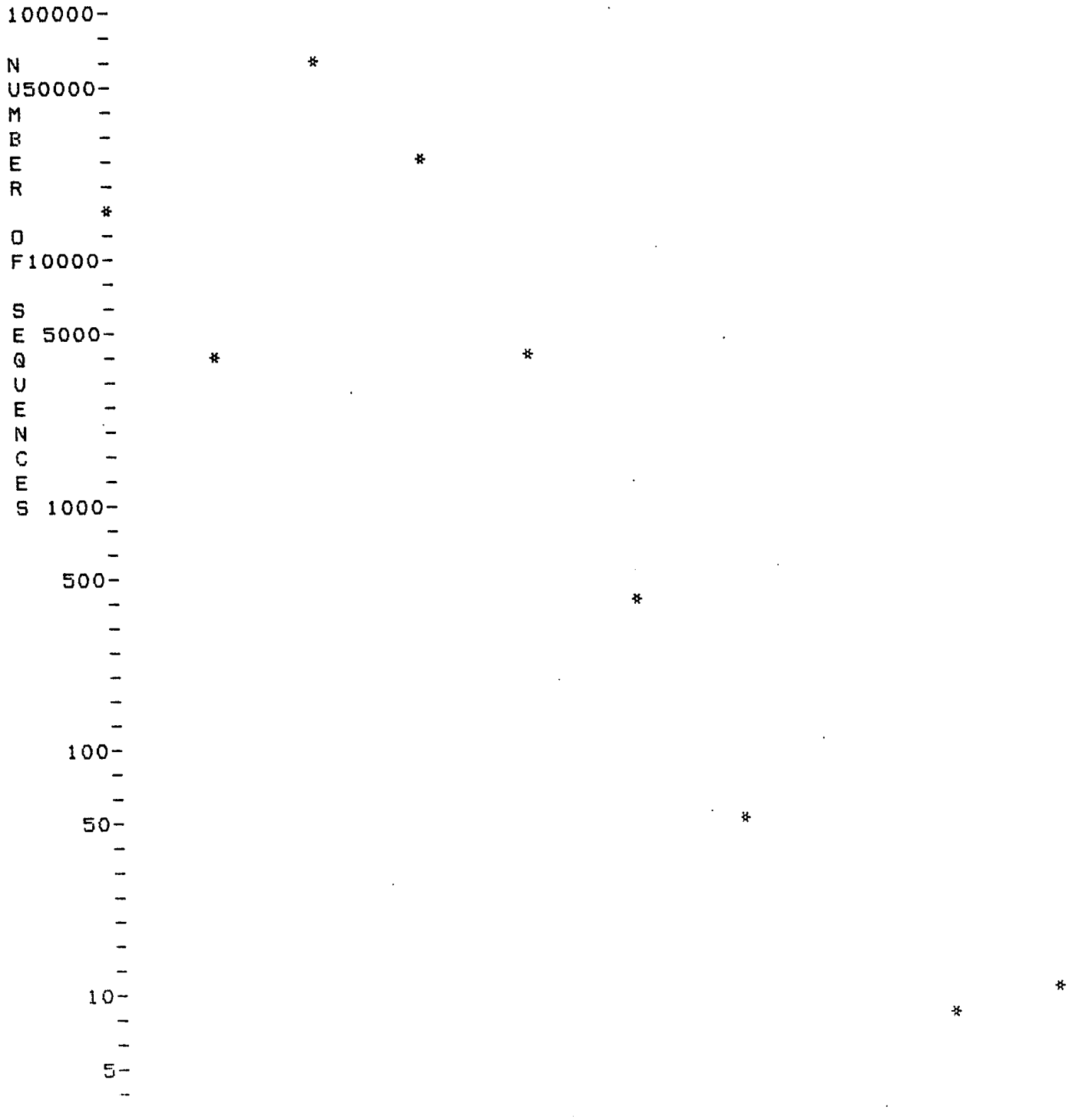
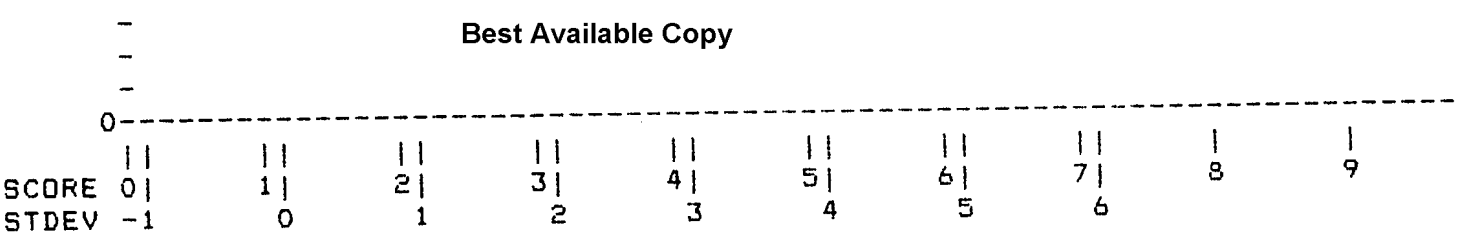
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-18.res made by alexk on Thu 25 Feb 93 10:37:20-PST.

Query sequence being compared: CELSA-18 (1-15)
Number of sequences searched: 94553
Number of scores above cutoff: 3965

Results of the initial comparison of CELSA-18 (1-15) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	3	1.00

Times:	CPU	Total Elapsed
	00:03:29.06	00:07:15.00

Number of residues:	25433612
Number of sequences searched:	94553
Number of scores above cutoff:	3965

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 6 standard deviations above mean ****					
1.	PPD1_BOVIN	PHOSPHODIESTERASE I (EC 3.1.4	61	9	9	6.98	0
2.	A25274	Phosphodiesterase I - Bovine	61	9	9	6.98	0
3.	A41179	*Protein kinase PC-1 - Bovine	289	9	9	6.98	0
4.	PC1_MOUSE	PLASMA-CELL MEMBRANE GLYCOPRO	871	9	9	6.98	0
5.	PC1_HUMAN	PLASMA-CELL MEMBRANE GLYCOPRO	873	9	9	6.98	0
6.	A27410	Plasma cell membrane protein	905	9	9	6.98	0
7.	S21706	*Pyrophosphatase - Human	925	9	9	6.98	0
8.	A39216	*Plasma cell membrane protein	925	9	9	6.98	0
		**** 5 standard deviations above mean ****					
9.	A37258	Hypothetical protein, 13K - M	115	8	8	5.98	0
10.	A28336	Hypothetical protein, 13K - M	115	8	8	5.98	0
11.	A27498	Coagulation Factor V precurso	1600	8	8	5.98	0
12.	FA5_HUMAN	COAGULATION FACTOR V PRECURSO	2224	8	8	5.98	0
13.	A28028	Coagulation Factor V precurso	2224	8	8	5.98	0
14.	TEGU_HUMAN	LARGE TEGUMENT PROTEIN	2763	8	9	5.98	0

**** 3 standard deviations above mean ****

16. B32268	*Carcinoembryonic antigen pre	120	6	6	3.99	0
17. PQ0328	Mucin-like peptide - Human (f	141	6	6	3.99	0
18. SODC_HAEPA	SUPEROXIDE DISMUTASE PRECURSO	187	6	6	3.99	0
19. SODC_HAEIN	SUPEROXIDE DISMUTASE LIKE PRO	187	6	6	3.99	0
20. B41654	*Superoxide dismutase (Cu-Zn)	187	6	6	3.99	0
21. A41654	*Superoxide dismutase (Cu-Zn)	187	6	6	3.99	0
22. P83190	[delta 1-5][Arg358] Alpha 1-a	390	6	6	3.99	0
23. P83189	[Ala357, Arg358] Alpha 1-anti	395	6	6	3.99	0
24. P40134	Sequence of human alpha-1-ant	418	6	6	3.99	0
25. P94665	Human alpha-1-antitrypsin as	418	6	6	3.99	0
26. FUCP_ECOLI	L-FUCOSE PERMEASE.	438	6	6	3.99	0
27. WQECFP	Fucose permease - Escherichia	438	6	6	3.99	0
28. GSH1_ECOLI	GLUTAMATE--CYSTEINE LIGASE (E	518	6	6	3.99	0
29. SYECEC	Glutamate--cysteine ligase -	518	6	6	3.99	0
30. TETO_CAMJE	TETRACYCLINE RESISTANCE PROTE	637	6	6	3.99	0
31. A29809	Tetracycline resistance prote	637	6	6	3.99	0
32. TETO_STRMU	TETRACYCLINE RESISTANCE PROTE	639	6	6	3.99	0
33. TETO_CAMCO	TETRACYCLINE RESISTANCE PROTE	639	6	6	3.99	0
34. S06388	*Tetracycline resistance prot	639	6	6	3.99	0
35. A31098	Tetracycline resistance prote	639	6	6	3.99	0
36. CR72_BACTI	72 KD CRYSTAL PROTEIN (DELTA	643	6	6	3.99	0
37. P91462	67-kD protein toxin.	643	6	6	3.99	0
38. DPOL_HPBV4	DNA POLYMERASE (EC 2.7.7.7).	730	6	6	3.99	0
39. DPOL_HPBVZ	DNA POLYMERASE (EC 2.7.7.7) (	750	6	6	3.99	0
40. JDVLVH	DNA-directed DNA polymerase -	750	6	6	3.99	0
41. DPOM_HPBVY	DNA POLYMERASE (EC 2.7.7.7) (	832	6	6	3.99	0
42. DPOL_HPBVY	DNA POLYMERASE (EC 2.7.7.7) (	832	6	6	3.99	0
43. DPOL_HPBVA	DNA POLYMERASE (EC 2.7.7.7).	832	6	6	3.99	0
44. S20748	*Hypothetical protein (preS1,	832	6	6	3.99	0
45. S20757	*Hypothetical protein (pre S1	832	6	6	3.99	0
46. JDVLA1	DNA-directed DNA polymerase -	832	6	6	3.99	0
47. JDVLVB	DNA-directed DNA polymerase -	832	6	6	3.99	0
48. JDVLVA	DNA-directed DNA polymerase -	832	6	6	3.99	0
49. JDVLVS	DNA-directed DNA polymerase -	842	6	6	3.99	0
50. DPOL_HPBVR	DNA POLYMERASE (EC 2.7.7.7).	843	6	6	3.99	0

No alignments saved.

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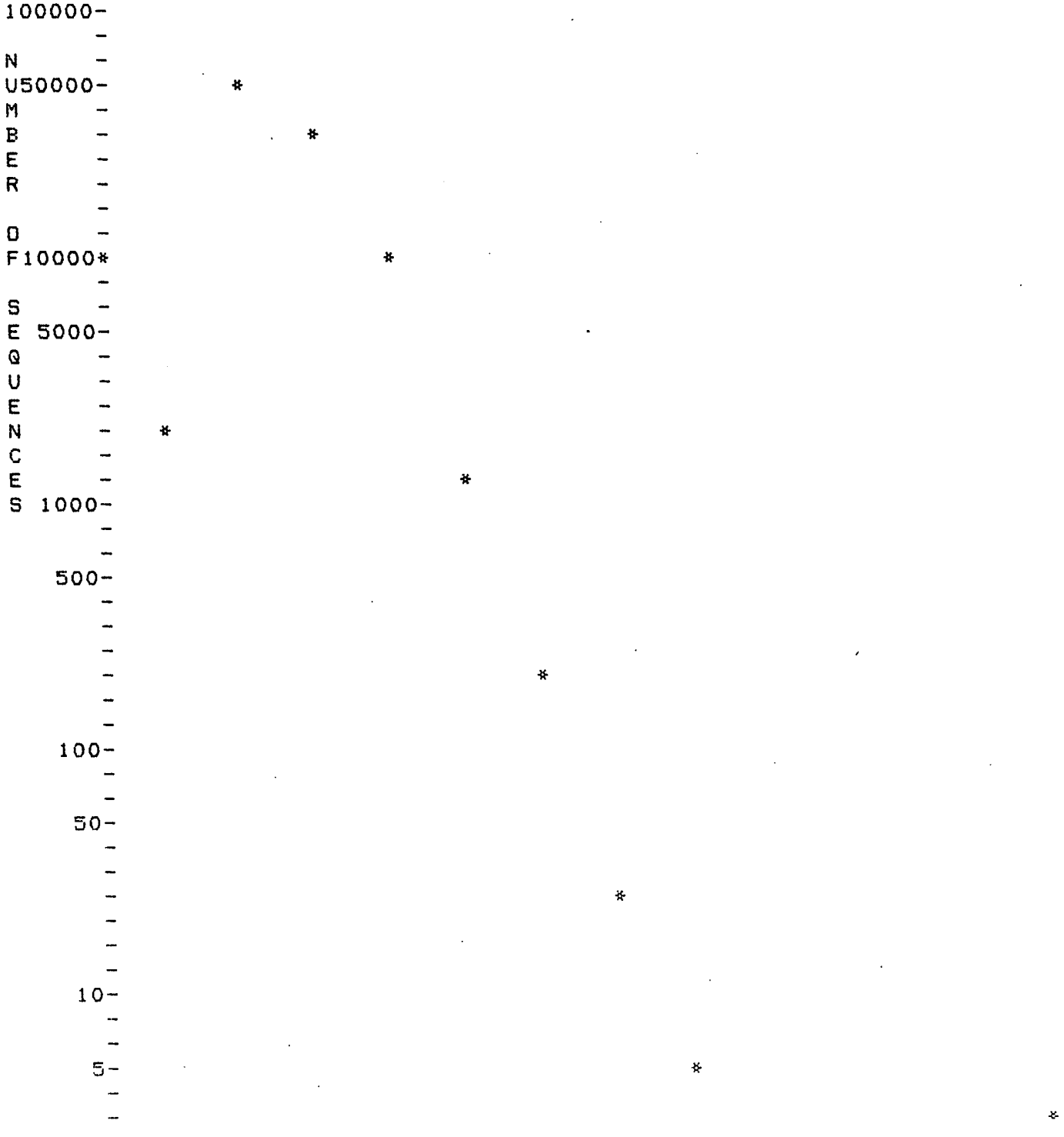
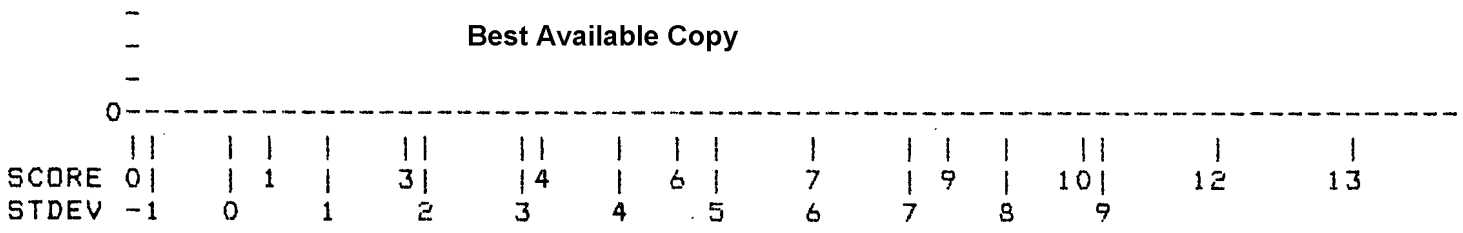
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file celsa-19.res made by alexk on Thu 25 Feb 93 10:37:29-PST.

Query sequence being compared: CELSA-19 (1-22)
Number of sequences searched: 94553
Number of scores above cutoff: 4944

Results of the initial comparison of CELSA-19 (1-22) with:
Data bank : A-GeneSeq 9, all entries
Data bank : PIR 34, all entries
Data bank : Swiss-Prot 23, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	5	Joining penalty	20
Gap penalty	1.00	Window size	5
Gap size penalty	0.26		
Cutoff score	0		
Randomization group	0		
Initial scores to save	50	Alignments to save	0
Optimized scores to save	0	Display context	0

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	3	1.06

Times:	CPU	Total Elapsed
	00:03:41.96	00:07:24.00

Number of residues: 25433612
Number of sequences searched: 94553
Number of scores above cutoff: 4944

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 10 standard deviations above mean ****					
1.	PC1_HUMAN	PLASMA-CELL MEMBRANE GLYCOPRO	873	13	14	10.41	0
2.	S21706	*Pyrophosphatase - Human	925	13	14	10.41	0
3.	A39216	*Plasma cell membrane protein	925	13	14	10.41	0
		**** 9 standard deviations above mean ****					
4.	PC1_MOUSE	PLASMA-CELL MEMBRANE GLYCOPRO	871	12	13	9.46	0
5.	A27410	Plasma cell membrane protein	905	12	13	9.46	0
		**** 5 standard deviations above mean ****					
6.	S20728	*Myosin light chain - Slime m	150	8	8	5.68	0
7.	MLE_DICDI	MYOSIN, ESSENTIAL LIGHT CHAIN	166	8	8	5.68	0
8.	A28127	Myosin light chain, nonmuscle	166	8	8	5.68	0
9.	J00367	Hypothetical protein 332, plc	332	8	9	5.68	0
		**** 4 standard deviations above mean ****					
10.	PHA3_FREDI	C-PHYCOCYANIN-3 ALPHA CHAIN.	162	7	8	4.73	0
11.	S05712	Phycocyanin 3 alpha chain - C	162	7	8	4.73	0
12.	VA35_VACCC	PROTEIN A35	174	7	8	4.77	0

14. CY1_NEUCR	CYTOCHROME C1, HEME PROTEIN P	332	7	7	4.73	0
15. A27187	Cytochrome c1, heme protein p	332	7	7	4.73	0
16. JN0260	*Enterobacterial common antig	348	7	7	4.73	0
17. YIFC_ECOLI	HYPOTHETICAL 39.6 KD IN RFE 3	349	7	7	4.73	0
18. PAT1_SOLTU	PATATIN B1 PRECURSOR (POTATO	377	7	7	4.73	0
19. S05593	Patatin (clone pPATB1) - Pota	377	7	7	4.73	0
20. PAT5_SOLTU	PATATIN T5 PRECURSOR (POTATO	386	7	7	4.73	0
21. PAT0_SOLTU	PATATIN PRECURSOR (POTATO TUB	386	7	7	4.73	0
22. A26017	Patatin T5 precursor - Potato	386	7	7	4.73	0
23. JS0624	Fatty acid beta oxidation mul	391	7	7	4.73	0
24. VGL2_CVMJH	E2 GLYCOPROTEIN PRECURSOR (SP	1235	7	7	4.73	0
25. VGIHMJ	E2 glycoprotein precursor - M	1235	7	7	4.73	0
26. VGL2_CVMA5	E2 GLYCOPROTEIN PRECURSOR (SP	1324	7	7	4.73	0
27. VGIH59	E2 glycoprotein precursor - M	1324	7	7	4.73	0
28. VGL2_CVM4	E2 GLYCOPROTEIN PRECURSOR (SP	1376	7	7	4.73	0
29. VGIHJ2	E2 glycoprotein precursor - M	1376	7	7	4.73	0
	**** 3 standard deviations above mean ****					
30. R13137	GPIb alpha peptide fragment.	15	6	7	3.79	0
31. THN6_HORVU	LEAF-SPECIFIC THIONIN (CLONE	46	6	6	3.79	0
32. S00825	Thionin BTH6, leaf - Barley	46	6	6	3.79	0
33. C551_ECTHA	CYTOCHROME C551.	78	6	7	3.79	0
34. CCER51	Cytochrome c551 - Ectothiorho	78	6	7	3.79	0
35. IMMC_ECOLI	IMMUNITY PROTEIN FOR CLOACIN.	85	6	6	3.79	0
36. B28585	Immunity protein - Escherichi	85	6	6	3.79	0
37. IMECP3	Immunity protein - Escherichi	85	6	6	3.79	0
38. FKBP_NEUCR	FK506-BINDING PROTEIN (FKBP)	120	6	6	3.79	0
39. S11090	*FK506-binding protein - Neur	120	6	6	3.79	0
40. THNL_HORVU	LEAF-SPECIFIC THIONIN PRECURS	137	6	7	3.79	0
41. THN4_HORVU	LEAF-SPECIFIC THIONIN PRECURS	137	6	7	3.79	0
42. S07648	Thionin precursor, leaf (clon	137	6	7	3.79	0
43. MLR_PHYPO	MYOSIN REGULATORY LIGHT CHAIN	147	6	7	3.79	0
44. S17769	*3-Dehydroquinase - Mycobacte	147	6	6	3.79	0
45. A29910	Myosin calcium-binding light	147	6	7	3.79	0
46. S09470	*Inter-alpha-trypsin inhibito	151	6	8	3.79	0
47. PHEA_MASLA	PHYCOERYTHROCYANIN ALPHA CHAI	162	6	7	3.79	0
48. PHCA_SYNPW	C-PHYCOCYANIN ALPHA CHAIN.	162	6	7	3.79	0
49. PHA2_FREDI	C-PHYCOCYANIN-2 ALPHA CHAIN.	162	6	7	3.79	0
50. J00764	*Phycoerythrocyanin alpha cha	162	6	7	3.79	0

No alignments saved.

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3. 5,003,047, Mar. 26, 1991, Method for purifying biologically active ligate; Martin L. Yarmush, et al., 530/413, 412, 421, 427 [IMAGE AVAILABLE]

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U.S. Patent & Trademark Office LOGOFF AT 14:10:12 ON 26 FEB 93

TABLE 4. Peptide sequences for Autotaxin.

PEPTIDE NO.	AMINO ACID SEQUENCE	SEQ ID: NO:	NAME
1.	WHVAAN	SEQ ID NO:1	ATX 18
2.	PXLDVYK	SEQ ID NO:2	ATX 19
3.	YPAFK	SEQ ID NO:3	ATX 20
4.	QAEVS	SEQ ID NO:4	ATX 24
5.	PEEVTXPNYL	SEQ ID NO:5	ATX 29
6.	YDVPWNETI	SEQ ID NO:6	ATX 47
7.	SPPFENINLY	SEQ ID NO:7	ATX 48
8.	GGQPLWITATK	SEQ ID NO:8	ATX 100
9.	VNSMQTVFVGY-GPTFK	SEQ ID NO:9	ATX 101
10.	DIEHLTSLDFFR	SEQ ID NO:10	ATX 102
11.	TEFLSNYLTNVDD-ITLVPGTLGR	SEQ ID NO:11	ATX 103
12.	QYLHQYGSS	SEQ ID NO:26	ATX 37
13.	VLNYF	SEQ ID NO:27	ATX 39
14.	YLNAT	SEQ ID NO:28	ATX 40
15.	HLLYGRPAVLY	SEQ ID NO:29	ATX 41
16.	SYPEILTPADN	SEQ ID NO:30	ATX 44
17.	XYGFLFPPYLSSSP	SEQ ID NO:31	ATX 53
18.	TFPNLYVF/LAQGLYWS	SEQ ID NO:32	ATX 59
19.	VNVISGPIFDYDYDGLH/A-DTEDK	SEQ ID NO:33	ATX 104

Peptide numbers 1-7 refer to peaks numbered in FIG. 11. Peptide numbers 12-18 refer to peptides purified from the preparation which yielded peptide numbers 1-7. Peptides 8-11 and 19, are from a separate purification, not shown in FIG. 11.

X refers to potentially glycosylated residues.

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     FILE 'REGISTRY' ENTERED AT 13:34:37 ON 26 FEB 93
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L2             0 S DIEHLTSLDFFR/SQSP

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COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
                                                 ENTRY    SESSION
FULL ESTIMATED COST                              26.20      26.46

STN INTERNATIONAL LOGOFF AT 13:36:24 ON 26 FEB 93
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